Run on:

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perfect score:
sequence: scoring table:

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Page 1
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OM nucleic - nucleic search, using sw model
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Maximum DB seq length: 2000000000
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.
                                                                                                                                                                                                                                                                                                                                                                                Score
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               published_Applications_NA:*
1: /cgn2_6/ptodata/1/pubpna/USO1_NEW_PUB.seq:*
2: /cgn2_6/ptodata/1/pubpna/USO6_NEW_PUB.seq:*
2: /cgn2_6/ptodata/1/pubpna/USO6_NEW_PUB.seq:*
3: /cgn2_6/ptodata/1/pubpna/USO6_NEW_PUB.seq:*
4: /cgn2_6/ptodata/1/pubpna/USO7_NEW_PUB.seq:*
5: /cgn2_6/ptodata/1/pubpna/USO8_NEW_PUB.seq:*
6: /cgn2_6/ptodata/1/pubpna/USO8_NEW_PUB.seq:*
7: /cgn2_6/ptodata/1/pubpna/USO8_PUBCOMB.seq:*
9: /cgn2_6/ptodata/1/pubpna/USO9_PUBCOMB.seq:*
10: /cgn2_6/ptodata/1/pubpna/USO9_PUBCOMB.seq:*
11: /cgn2_6/ptodata/1/pubpna/USO9_PUBCOMB.seq:*
12: /cgn2_6/ptodata/1/pubpna/USO9_PUBCOMB.seq:*
13: /cgn2_6/ptodata/1/pubpna/USO9_PUBCOMB.seq:*
14: /cgn2_6/ptodata/1/pubpna/USO9_PUBCOMB.seq:*
15: /cgn2_6/ptodata/1/pubpna/USO9_PUBCOMB.seq:*
16: /cgn2_6/ptodata/1/pubpna/USO9_PUBCOMB.seq:*
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Copyright (c) 1993 - 2003 Compugen Ltd.
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     3 US-10-081-817-19
2 US-10-059-579-120
2 US-10-059-579-120
2 US-10-27-632-196114
3 US-10-237-435-6
4 US-10-237-435-6
12 US-10-237-24-07
3 US-09-989-723-407
5 US-09-989-727-407
5 US-09-989-737-407
5 US-09-989-738-407
5 US-09-981-03-407
5 US-09-991-163-407
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                      Sequence 19, Appl
Sequence 120. App
Sequence 196114,
Sequence 6, Appli
Sequence 407, App
                                                                                                                                                                                                                                                                                                                                                                                                            Description
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US-10-081-817-19
US-10-081-817-19
Sequence 19, Application US/10081817
Sequence 19, Application US20020183501A1

publication No. US20020183501A1

publication No. US20020183501A1

publication No. US20020183501A1

APPLICANT: Porter, Dale
APPLICANT: SQrc1, Dennis
APPLICANT: Krop, Ian
APPLICANT: Krop, Ian
APPLICANT: Krop, Ian
APPLICANT: NOWER: US/10/081,817

FILE REFERENCE: 00530-094001

FILE REFERENCE: 00530-09401

FILE APPLICATION NUMBER: 60/270,973

PRIOR APPLICATION NUMBER: 60/270,973

PRIOR APPLICATION NUMBER: 60/251,908

PRIOR APPLICATION NUMBER: 60/251,908

PRIOR APPLICATION NUMBER: 60/251,908

PRIOR FILING DATE: 2002-01-25

PRI
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US-10-081-817-19
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                                                                                                                   Вþ
                                                                                                                                                                                                                Query Match 92.4
Query Match Similarity 97.8
Best Local Similarity 97.8
Matches 539; Conservative
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                                                                                                                           92.4%;
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US-09-989-7298-407
US-09-989-735-407
US-09-989-730-407
US-09-991-181-407
US-09-991-181-407
US-09-991-181-407
US-09-991-687-407
US-09-997-428-407
US-09-997-428-407
US-09-997-428-407
US-09-997-428-407
US-09-997-428-407
US-09-997-438-407
US-09-991-181-407
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Result No.

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GENERAL INFORMATION:

GENERAL INFORMATION:

APPLICANT: THE JOHNS HOPKINS UNIVERSITY SCHOOL OF MEDICINE

APPLICANT: SUKUMAR; SAFRAWALI

APPLICANT: EVRON, Ella

APPLICANT: DOOLEY, William C.

APPLICANT: DAVIDSON, NANCY

APPLICANT: FACKLER; MARY JO.

TITLE OF INVENTION: ABERRANTLY METHYLATED GENES AS MARKERS OF

FILE REFERENCE: JHU1630-1

CURRENT APPLICATION NUMBER: US/10/059,579

CURRENT FILING DATE: 2003-02-03

PRIOR APPLICATION NUMBER: US 09/771,357

PRIOR APPLICATION NUMBER: US 09/771,357
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                                                                                                                                           NAME/KEY: misc_feature; LOCATION: (359)..(359); OTHER INFORMATION: n is US-10-059-579-120
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                                                                                                                                                                                                                                          NUMBER OF SEQ ID NOS: 136
SOFTWARE: PatentIn version
SEQ ID NO 120
LENGTH: 1794
                                                                                                  Query Match
Best Local
                                                                                      Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Publication No.
                                                                                                                                                                                                              TYPE: DNA
ORGANISM: Homo sapiens
                                                                                                                                                                                                    FEATURE:
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  190 GAGGGAAGCTCCCCTCACCCGGCCCAGCCCTGCAGGGGGGCGCGTGGGGTCAGACCGCAA
                                                                                    354;
                                                                                                Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Application US/10059579
p. US20030138783A1
                                                                                    Conservative
                                                                                                                                                         is any nucleotide
                                                                                                61.4%;
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                                                                                 Score 338.4; DB 12;
Pred. No. 1.3e-64;
0; Mismatches 6;
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                                                                                    Indels
                                                                                                             Length 1794;
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Sequence 196114, Application US/10027632
GENERAL INFORMATION:
APPLICANT: Wang, David G.
TITLE OF INVERVION: Identification and Mapping of Single Nucleotide
TITLE OF INVERVION: Polymorphisms in the Human Genome
FILE REFERENCE: 108827.129
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CURRENT FILING DATE: 2002-04-30
PRIOR APPLICATION NUMBER: US 60/218,006
PRIOR FILING DATE: 2000-07-12
PRIOR APPLICATION NUMBER: US 60/198,676
PRIOR FILING DATE: 2000-04-20
PRIOR PPLICATION NUMBER: US 60/193,483
PRIOR FILING DATE: 2000-03-29
PRIOR APPLICATION NUMBER: US 60/185,218
PRIOR FILING DATE: 2000-02-24
PRIOR FILING DATE: 2000-02-24
PRIOR FILING DATE: 1999-11-23
PRIOR FILING DATE: 1999-11-23
PRIOR APPLICATION NUMBER: US 60/156,358
PRIOR FILING DATE: 1999-09-28
PRIOR APPLICATION NUMBER: US 60/156,358
PRIOR APPLICATION NUMBER: US 60/146,002
PRIOR APPLICATION NUMBER: US 60/146,002
PRIOR FILING DATE: 1999-08-09
PRIOR FILING DATE: 1999-08-09
PRIOR FILING DATE: 1999-08-09
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SOFTWARE: FastSEQ for V
SEQ ID NO 196114
LENGTH: 533
TYPE: DNA
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                                                                                                                                                                                                               Query Match
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                                                                                                                                                      1 CGGCCGGGGAGCCGGCCGGGATGAGGCCTGATCGTCCCTGGCGCCTCCACCTCCCCAGG
                                                                                                                                                                                                                 Similarity
                                             CGCAGAAGGCGCCCACGAGGACCCCCCAGTGCCCGACGTTGCCACGGTCTGGGATCAGAGG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    င္ပ
                                                                                    CGCAGAAGGCGCCCACGAGGACCCCCAGTGCCCGACGTTGCCACGGTCTGGGATCAGAGG
                                                                                                                                           CGGCCGGGGAGGCGGCGGGAGTGAGGCCTGATCGTCCCTGGCGCGCCTCCACCTCCCCAGG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           င္ပ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  AGAAGCCTCGTGGCCTTGCCCGGGCAGCCGCAGGTTCCCCGCGCGCCCCGAGCCCCCGCG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            CTTCCCACGCCCGCCGCCGCAGCAGGAAGTTGGCCAGGGCACGGCCGTGAGCGGAGCG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        CTTCCCAGGGCCCGCCGGCCGCAGGAGGTTGGCCAGGGCACGGCCGTGAGCGGAGCG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                AGGGCCCCAGCGCCTGCCAAGAGGAAGTCCTCGAGGCCCGGGCAGGGAAGGGGGCACGGG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TCCCTCACCNG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    AGGGCCCCAGCGCCTGCCAAGAGGAAGTCCTCGAGGCCCCGGGCAGGGAAGGGGGCACGGG
                              CACGGGACCAGGGAGCCAGGAACTGCGCCGCCC----CGCCCTGCCTGGCGCGA-GGAAGC
                                                                                                                                                                                                  Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      551
                                                                                                                                                                                                               26.1%;
  190
                                                                                                                                                                                                  0;
                                                                                                                                                                                                 Score 143.6; DB 13; Pred. No. 1.5e-22; 0; Mismatches 5;
                                                                                                                                                                                                    Indels
                                                                                                                                                                                                                             Length 533
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                                                                                                                                                                                                  Gaps
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                                                         179
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                              14
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RESULT 4
US-10-237-435-6
US-10-237-435-6
US-10-237-435-6
Sequence 6, Application US/10237435
Sequence 10, US20030124580A1
Publication No. US20030124580A1

Publication No. US20030124580A1

APPLICANT: Spiro, Peter A.
APPLICANT: MUTTY, LYND SURFACTANT MOLECULES
FILE REFERENCE: PB-0019 US
FILING DATE: 2002-09-06
CURRENT APPLICATION NUMBER: 60/317,822
PRIOR APPLICATION NUMBER: 60/317,822
PRIOR FILING DATE: 09-07-2001
PRIOR FILING PRIOR DESCRIPTION SECUENCES
SEQ ID NO 6
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Вþ
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US-10-210-951-27
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Query Match 21.1%; Score 116; DB 14; Length 56 Best Local Similarity 100.0%; Pred. No. 1.3e-16; Best Local Similarity 0; Mismatches 0; Indels Matches 116; Conservative 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Sequence 27, Application US/10210951 publication No. US20030170228A1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TYPE: DNA ORGANISM: Homo sapiens
FITLE DE INVENTION:

FILE REPERBUCE: P2931R12: US/10/210,951

CURRENT APPLICATION NUMBER: US/10/216.99

CURRENT FILING DATE: 2002-08-02

PRIOR APPLICATION NUMBER: 60/0146.99

PRIOR PELLORIUN UNMBER: 60/026.943

PRIOR APPLICATION NUMBER: 60/059121

PRIOR FILING DATE: 1996-09-23

PRIOR PELLORIUN NUMBER: 60/059352

PRIOR PILING DATE: 1997-09-19

PRIOR APPLICATION NUMBER: 60/05237

PRIOR APPLICATION NUMBER: 60/062037

PRIOR APPLICATION NUMBER: 60/062037
                                                                                                                                                                                                                                                                                                                                                                                                                                                     APPLICANT:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Goddard, Audrey
Godowski, Paul J.
Gurney, Austin L.
Hillan, Kenneth J.
Marsters, Scot A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   pitti, Robert M.
Roy, Margaret Ann
Smith, Victoria
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PRIOR ETLING DATE: 1997-10-10

PRIOR APPLICATION NUMBER: 60/063755

PRIOR APPLICATION NUMBER: 60/063045

PRIOR APPLICATION NUMBER: 60/063046

PRIOR APPLICATION 1997-10-24

PRIOR APPLICATION 10MBER: 60/06511

PRIOR APPLICATION 10MBER: 60/066511

PRIOR APPLICATION 10MBER: 60/066772

PRIOR FILING DATE: 1997-11-24

PRIOR PRIOR PRIOR DATE: 1997-11-24

PRIOR PRIOR PRIOR DATE: 1997-11-24

PRIOR PRIOR PRIOR DATE: 1997-11-24

PRIOR PRIOR DATE: 1997-11-24

PRIOR PRIOR DATE: 1997-11-24

PRIOR PRI
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APPLICANT: HOY, MAIGATET AND
APPLICANT: Tumas, Daniel
APPLICANT: Tumas, Daniel
APPLICANT: Watanabe, Colin K.
APPLICANT: Watanabe, Colin K.
APPLICANT: Watlanabe, P. Mickey
APPLICANT: Watliams.
APPLICANT: Wood, William I.
APPLICANTON UNMER: Bencoding the Same
TITLE OF INVENTION. Acids Encoding the Same
TITLE OF INVENTION NUMBER: 00/049787
CURRENT APPLICATION NUMBER: 00/049787
PRIOR APPLICATION NUMBER: 00/062250
PRIOR APPLICATION NUMBER: 00/065186
PRIOR FILING DATE: 1997-10-12
PRIOR FILING DATE: 1997-11-12
PRIOR FILING DATE: 1997-11-12
PRIOR APPLICATION NUMBER: 60/065311
PRIOR APPLICATION NUMBER: 60/065311
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        RESULT 6
US-09-989-722-407
US-09-989-722-407, A
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 PPLICANT:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            INFORMATION
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Similarity 100.0%; Pred. No. 1.9e-08;
78; Conservative 0; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         07, Application US/09989722
US20020072067A1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Fong, Sherman
Fong, Sherman
Gerber, Hanspeter
Gerritsen, Mary E.
Goddard, Audrey
Goddwski, Paul J.
Godowski, Paul J.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Baker, Kevin P.
Botstein, David
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Desnoyers, Luc
Eaton, Dan L.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Gurney, Austin L.
Kljavin, Ivar J.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Napier, Mary A.
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PRIOR APPLICATION NUMBER: 60/089532 PRIOR PILING DATE: 1998-06-17 PRIOR APPLICATION NUMBER: 60/089538 PRIOR FILING DATE: 1998-06-17 PRIOR APPLICATION NUMBER: 60/089598 PRIOR FILING DATE: 1998-06-17 PRIOR APPLICATION NUMBER: 60/089599 PRIOR FILING DATE: 1998-06-17 PRIOR APPLICATION NUMBER: 60/089603 PRIOR FILING DATE: 1998-06-18 PRIOR APPLICATION NUMBER: 60/089907 PRIOR APPLICATION NUMBER: 60/089907 PRIOR APPLICATION NUMBER: 60/089908 PRIOR FILING DATE: 1998-06-18 PRIOR APPLICATION NUMBER: 60/089907 PRIOR FILING DATE: 1998-06-19 PRIOR APPLICATION NUMBER: 60/089907 PRIOR FILING DATE: 1998-06-19 PRIOR APPLICATION NUMBER: 60/089948 PRIOR FILING DATE: 1998-06-19 PRIOR APPLICATION NUMBER: 60/089952 PRIOR FILING DATE: 1998-06-29 PRIOR APPLICATION NUMBER: 60/090246 PRIOR APPLICATION NUMBER: 60/090252 PRIOR APPLICATION NUMBER: 60/090252 PRIOR APPLICATION NUMBER: 60/090252 PRIOR APPLICATION NUMBER: 60/090244 PRIOR APPLICATION NUMBER: 60/090252 PRIOR FILING DATE: 1998-06-24 PRIOR APPLICATION NUMBER: 60/090435 PRIOR APPLICATION NUMBER: 60/090445 PRIOR APPLICATION NUMBER: 60/090461 PRIOR APPLICATION NUMBER: 60/090462 PRIOR APPLICATION NUMBER: 60/090557 PRIOR PILING DATE: 1998-06-24 PRIOR APPLICATION NUMBER: 60/090557 PRIOR PILING DATE: 1998-06-25 PRIOR APPLICATION NUMBER: 60/090567 PRIOR APPLICATION NUMBER: 60/090567 PRIOR PILING DATE: 1998-06-25 PRIOR APPLICATION NUMBER: 60/090567 PRIOR APPLICATION NUMBER: 60/090569 PRIOR FILING DATE: 1998-06-25 PRIOR PILING DATE: 1998-06-25 PRIOR APPLICATION NUMBER: 60/090669 PRIOR FILING DATE: 1998-06-25 PRIOR APPLICATION NUMBER: 60/090669 PRIOR FILING DATE: 1998-06-25 PRIOR APPLICATION NUMBER: 60/0			
### PELLICATION NUMBER: 60/08 ### EILING DATE: 1998-06-17 ### PELLICATION NUMBER: 60/08 ### PELL			
NUMBER: 60/06 1998-06-17 NUMBER: 60/07 1998-06-17 1998-06-17 NUMBER: 60/08 1998-06-17 NUMBER: 60/08 1998-06-17 NUMBER: 60/08 1998-06-18 1998-06-18 1998-06-18 1998-06-18 1998-06-18 1998-06-18 1998-06-18 1998-06-19 1998-06-19 1998-06-19 1998-06-19 1998-06-29 NUMBER: 60/08 1998-06-29 NUMBER: 60/08 1998-06-24 NUMBER: 60/08 1998-06-25 NUMBER: 60/08 1998-06-26 NUMBER: 60/08	IOR	PRIOR	PRIOR
NUMBER: 60/06 1998-06-17 NUMBER: 60/07 1998-06-17 1998-06-17 NUMBER: 60/08 1998-06-17 NUMBER: 60/08 1998-06-17 NUMBER: 60/08 1998-06-18 1998-06-18 1998-06-18 1998-06-18 1998-06-18 1998-06-18 1998-06-18 1998-06-19 1998-06-19 1998-06-19 1998-06-19 1998-06-29 NUMBER: 60/08 1998-06-29 NUMBER: 60/08 1998-06-24 NUMBER: 60/08 1998-06-25 NUMBER: 60/08 1998-06-26 NUMBER: 60/08	PPLICATION TILING DATE PPLICATION TON TON TON TON TON TON TON TON TON T	APPLICATION FILING DATE APPLICATION FILING DATE FILING DATE APPLICATION FILING DATE APPLICATION FILING DATE APPLICATION FILING DATE FILING DATE APPLICATION FILING DATE FILING DATE APPLICATION FILING DATE FILING	APPLICATION FILING DATE APPLICATION APPLIC
	NUMBER: 60/08 1198-06-25 1198-06-25 1198-06-25 1198-06-25 1198-06-25 NUMBER: 60/09 1198-06-25 NUMBER: 60/09 1198-06-26 NUMBER: 60/09 1198-06-26 NUMBER: 60/09 1198-06-26 NUMBER: 60/09 1198-07-01 1198-07-01	NUMBER: 60/09 1998-06-24 NUMBER: 60/09 1998-06-24 1998-06-24 1998-06-24 NUMBER: 60/09	NUMBER: 60/08 1998-06-17 NUMBER: 60/08 1998-06-18 NUMBER: 60/08 1998-06-18 NUMBER: 60/08 1998-06-18 NUMBER: 60/08 1998-06-19 1998-06-19 NUMBER: 60/08 1998-06-19 1998-06-19 1998-06-19 1998-06-19 1998-06-19 1998-06-19 1998-06-19 1998-06-19 1998-06-22 NUMBER: 60/02 1998-06-22 NUMBER: 60/05 1998-06-22 NUMBER: 60/05 1998-06-22 NUMBER: 60/05

PRIOR PRIOR

PRIOR PRIOR PRIOR PRIOR PRIOR

OR APPLICATION NUMBER: 60/089105
OR FILLING DATE: 1998-06-12
OR APPLICATION NUMBER: 60/089440
OR FILLING DATE: 1998-06-16
OR APPLICATION NUMBER: 60/089512
OR FILING DATE: 1998-06-16
OR APPLICATION NUMBER: 60/089514
OR FILING DATE: 1998-06-16

PRIOR PRIOR

OR FILING DATE: 1998-06-10
OR APPLICATION NUMBER: 60/088742
OR FILING DATE: 1998-06-10
OR APPLICATION NUMBER: 60/088810
OR FILING DATE: 1998-06-10
OR APPLICATION NUMBER: 60/088824
OR FILING DATE: 1998-06-10
OR APPLICATION NUMBER: 60/088826
OR APPLICATION NUMBER: 60/088828
OR FILING DATE: 1998-06-11
OR APPLICATION NUMBER: 60/088858
OR FILING DATE: 1998-06-11
OR APPLICATION NUMBER: 60/088861
OR FILING DATE: 1998-06-11
OR APPLICATION NUMBER: 60/088876
OR FILING DATE: 1998-06-11

PRIOR PRIOR

PRIOR PRIOR PRIOR PRIOR PRIOR PRIOR PRIOR

OR APPLICATION NUMBER: 60/088033
OR FILING DATE: 1998-06-04
OR APPLICATION NUMBER: 60/088326
OR FILING DATE: 1998-06-04
OR APPLICATION NUMBER: 60/088167
OR FILING DATE: 1998-06-05
OR APPLICATION NUMBER: 60/088202
OR FILING DATE: 1998-06-05
OR FILING DATE: 1998-06-05
OR APPLICATION NUMBER: 60/088212
OR FILING DATE: 1998-06-05
OR APPLICATION NUMBER: 60/088217
OR FILING DATE: 1998-06-05
OR APPLICATION NUMBER: 60/088217
OR FILING DATE: 1998-06-05
OR FILING DATE: 1998-06-09
OR APPLICATION NUMBER: 60/088734
OR FILING DATE: 1998-06-10
OR APPLICATION NUMBER: 60/088734
OR FILING DATE: 1998-06-10
OR APPLICATION NUMBER: 60/088734
OR FILING DATE: 1998-06-10

PRIOR

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APPLICATION NUMBER: 60/088030 FILING DATE: |1998-06-04

PRIOR PRIOR PRIOR

OR APPLICATION NUMBER: 60/088025
OR FILING DATE: 1998-06-04
OR FILING DATE: 1998-06-04
OR FILING DATE: 1998-06-04
OR APPLICATION NUMBER: 60/088028
OR FILING DATE: 1998-06-04
OR APPLICATION NUMBER: 60/08029
OR APPLICATION NUMBER: 60/08029
OR FILING DATE: 1998-06-04

PRIOR PRIOR PRIOR PRIOR PRIOR

PRIOR PRIOR PRIOR PRIOR PRIOR PRIOR PRIOR PRIOR

OR APPLICATION NUMBER: 60/087607
OR FILING DATE: 1998-06-02
OR FILING DATE: 1998-06-02
OR FILING DATE: 1998-06-02
OR APPLICATION NUMBER: 60/087759
OR FILING DATE: 1998-06-02
OR FILING DATE: 1998-06-02
OR FILING DATE: 1998-06-03
OR FILING DATE: 1998-06-03
OR APPLICATION NUMBER: 60/087827
OR FILING DATE: 1998-06-03
OR FILING DATE: 1998-06-04
OR FILING DATE: 1998-06-04

PRIOR PRIOR PRIOR PRIOR PRIOR

OR APPLICATION NUMBER: 60/078910
OR FILING DATE: 1998-03-20
OR APPLICATION NUMBER: 60/083322
OR FILING DATE: 1998-04-28
OR APPLICATION NUMBER: 60/084600
OR FILING DATE: 1998-05-07
OR APPLICATION NUMBER: 60/087106
OR FILING DATE: 1998-05-28
OR FILING DATE: 1998-05-28

FILING DATE: 1997-11-13
APPLICATION NUMBER: 60/066770
FILING DATE: 1997-11-24
APPLICATION NUMBER: 60/075945
FILING DATE: 1998-02-25

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PRIOR FILING DATE: 1998-07-02
PRIOR APPLICATION NUMBER: 60/091544
PRIOR APPLICATION UNMEER: 60/091519
PRIOR PELICATION UNMEER: 60/091519
PRIOR PELICATION UNMEER: 60/091626
PRIOR PELICATION UNMEER: 60/091626
PRIOR FILING DATE: 1998-07-02
PRIOR FILING DATE: 1998-07-02
PRIOR PLICATION UNMEER: 60/091978
PRIOR APPLICATION UNMEER: 60/091978
PRIOR APPLICATION UNMEER: 60/091982
PRIOR APPLICATION UNMEER: 60/091982
PRIOR APPLICATION UNMEER: 60/091982
PRIOR APPLICATION UNMEER: 60/091982
PRIOR APPLICATION UNMEER: 60/092182
PRIOR FILING DATE: 1998-07-07
PRIOR FILING DATE: 1998-07-07
PRIOR FILING DATE: 1998-07-07
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US-09-989-723-407
US-09-989-723-407
Sequence 407, App!
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Best Local S:
Matches 78
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APPLICANT: NOY. Timothy A.
APPLICANT: Tumas, Daniel N.
APPLICANT: Tumas, Daniel N.
APPLICANT: Withanabe, Colin K.
APPLICANT: Withanabe, P. Mickey
APPLICANT: Williams, P. Mickey
APPLICANT: Wood, William I.
APPLICANT: Zhang, Zemin
APPLICANT: Zhang, Zemin
APPLICANTON NUMBER: G0/049787
FILE REFERENCE: P2730P1C62
CURRENT APPLICATION NUMBER: 60/049787
PRIOR APPLICATION NUMBER: 60/049787
PRIOR APPLICATION NUMBER: 60/065250
PRIOR APPLICATION NUMBER: 60/065216
PRIOR APPLICATION NUMBER: 60/065311
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APPLICANT: Ashkenazi, Avi J.
APPLICANT: Baker, Kevin P.
APPLICANT: Botstein, David
APPLICANT: Desnoyers, Luc
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Similarity 100.0%; Pred. No. 1.
Significative 0; Mismatches
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Godowski, Paul J
Grimaldi, J. Christopher
Gurney, Austin L
Kijavin, Ivar J
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Gerritsen, Mary E.
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20020072092A1
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Paoni, Nicholas F.
Roy, Margaret Ann
Stewart, Timothy A.
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                                                                                                PRIOR APPLICATION NUMBER: 60/075945
PRIOR FILING DATE: 1998-02-25
PRIOR FILING DATE: 1998-03-20
PRIOR FILING DATE: 1998-05-28
PRIOR FILING DATE: 1998-05-28
PRIOR FILING DATE: 1998-05-28
PRIOR PLICATION NUMBER: 60/08760
PRIOR PRILING DATE: 1998-05-28
PRIOR PRILING DATE: 1998-06-02
PRIOR APPLICATION NUMBER: 60/08760
PRIOR PRILING DATE: 1998-06-02
PRIOR APPLICATION NUMBER: 60/08762
PRIOR APPLICATION NUMBER: 60/088021
PRIOR PRILING DATE: 1998-06-02
PRIOR PRILING DATE: 1998-06-04
PRIOR PRILING DATE: 1998-06-05
PRIOR PRILING DATE: 1998-06-10
PRIOR PRIOR PRILING DATE: 1998-06-10
PRIOR PRIOR PRILING DATE: 1998-06-10
PRIOR PRIOR PRICING DATE: 1998-06-1
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PRIOR FILLING DATE: 1998-06-17
PRIOR APPLICATION NUMBER: 60,008959
PRIOR FILLING DATE: 1998-06-17
PRIOR APPLICATION NUMBER: 60,008959
PRIOR FILLING DATE: 1998-06-18
PRIOR PELLING DATE: 1998-06-19
PRIOR PELLING DATE: 1998-06-29
PRIOR PELLING DATE: 1998-06-24
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PRIOR PELLING DATE: 1998-06-24
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PRIOR PELLING DATE: 1998-06-39
PRIOR PELLING DATE: 1998-06-39
PRIOR PELLING DATE: 1998-06-34
PRIOR PELLING DATE: 1998-06-36
PRIOR PELLING DATE: 1
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TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic TITLE OF INVENTION: Acids Encoding the Same FILE REFERENCE: P273091C56

CURRENT APPLICATION NUMBER: US/09/989,279

CURRENT FILING DATE: 2001-11-19

PRIOR PILING DATE: 1997-06-16

PRIOR FILING DATE: 1997-06-16

PRIOR RELICATION NUMBER: 60/06250

PRIOR APPLICATION NUMBER: 60/06250

PRIOR APPLICATION NUMBER: 60/06516

PRIOR PILING DATE: 1997-10-17

PRIOR APPLICATION NUMBER: 60/065311

PRIOR FILING DATE: 1997-11-13

PRIOR APPLICATION NUMBER: 60/066770

PRIOR FILING DATE: 1997-11-23

PRIOR APPLICATION NUMBER: 60/066770

PRIOR FILING DATE: 1997-11-24

PRIOR APPLICATION NUMBER: 60/075945

PRIOR APPLICATION NUMBER: 60/075945

PRIOR PILING DATE: 1998-02-25

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US-09-989-279-407
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PRIOR FILLING DATE: 1998-07-02
PRIOR APPLICATION NUMBER: 60/091626
PRIOR FILLING DATE: 1998-07-02
PRIOR APPLICATION NUMBER: 60/091633
PRIOR FILLING DATE: 1998-07-07
PRIOR APPLICATION NUMBER: 60/091978
PRIOR FILLING DATE: 1998-07-07
PRIOR APPLICATION NUMBER: 60/091982
PRIOR FILLING DATE: 1998-07-07
PRIOR APPLICATION NUMBER: 60/091982
PRIOR FILLING DATE: 1998-07-07
PRIOR APPLICATION NUMBER: 60/091982
PRIOR FILLING DATE: 1998-07-09
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APPLICANT: Baker, Kevin P.
APPLICANT: Botstein, David
APPLICANT: Botstein, David
APPLICANT: Desnoyers, Luc
APPLICANT: Eaton, Dan L.
APPLICANT: Fong, Sherman
APPLICANT: Fong, Sherman
APPLICANT: Gerber, Hanspeter
APPLICANT: Gerber, Hanspeter
APPLICANT: Goddard, Audrey
APPLICANT: Goddwski, Paul J.
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Best Local !
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Gerritsen, Mary E.
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Kljavin, Ivar J
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Stewart, Timothy A.
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20020072496A1
NUMBER: 60/078910
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PRIOR FILLING DATE: 1998-03-20
PRIOR APPLICATION UNMBER: 60/08322
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PRIOR FILLING DATE: 1998-05-07
PRIOR FILLING DATE: 1998-06-02
PRIOR FILLING DATE: 1998-06-02
PRIOR FILLING DATE: 1998-06-02
PRIOR PRILING DATE: 1998-06-02
PRIOR PRILING DATE: 1998-06-02
PRIOR PRILING DATE: 1998-06-03
PRIOR PRILING DATE: 1998-06-04
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PRIOR PRILING DATE: 1998-06-10
PRIOR PRILING DATE: 1998-06-11
PRIOR PRILING DATE: 1998-06-10
PRIOR PRILING DATE: 19

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APPLICANY: Roy, Margaret Ann
APPLICANY: Stewart, Timothy A.
APPLICANY: Stewart, Timothy A.
APPLICANY: Williams; P. Mickey
APPLICANY: Williams; P. Mickey
APPLICANY: Williams; P. Mickey
APPLICANY: Williams; P. Mickey
APPLICANY: Wood, William I.
APPLICANY: 
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US-09-989-727-407
Sequence 407, Application US/09989727
Patent No. US20020072497A1
GENERAL INFORMATION;
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PRIOR APPLICATION NUMBER: 60/091633
PRIOR FILING DATE: 1998-07-02
PRIOR APPLICATION NUMBER: 60/091978
PRIOR FILING DATE: 1998-07-07
PRIOR FILING DATE: 1998-07-07
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PRIOR FILING DATE: 1998-07-09
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APPLICANT: Baker. Kevin P.
APPLICANT: Baker. kevin P.
APPLICANT: Botsetán David
APPLICANT: Desnoyers, Luc
APPLICANT: Earton, Dan L.
APPLICANT: Ferrara Nappleone
APPLICANT: Fong, Sherman
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Gurney, Austin L.
Kljavin, Ivar J.
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Godowski, Paul J.
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PRIOR APPLICATION NUMBER: 60/087759
PRIOR APPLICATION NUMBER: 60/087759
PRIOR APPLICATION NUMBER: 60/088021
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PRIOR APPLICATION NUMBER: 60/088026
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PRIOR APPLICATION NUMBER: 60/088029
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FILING DATE: 1998-05-07
APPLICATION NUMBER: 60/
                                                      APPLICATION NUMBER: 60/089599 FILING DATE: 1998-06-17
                     NUMBER: 60/089600
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Query Match
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Matches 78
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Patent No.
GENERAL INF
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PRIOR FILING DATE: 1998-07-07
PRIOR EPLICATION NUMBER: 60/091982
PRIOR APPLICATION NUMBER: 60/091982
PRIOR APPLICATION NUMBER: 60/092182
PRIOR FILING DATE: 1998-07-09
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78; Conservative 0; Mismatches
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Baker, Kevin P.
Botstein, David
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Eaton, Dan L.
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Gerber, Hanspeter
Gerritsen, Mary E.
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Stewart, Timothy A.
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PRIOR FILING DATE: 1998-06-17
PRIOR APPLICATION NUMBER: 60/089653
PRIOR APPLICATION NUMBER: 60/089801
PRIOR APPLICATION NUMBER: 60/089908
PRIOR APPLICATION NUMBER: 60/089908
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PRIOR APPLICATION NUMBER: 60/089952
PRIOR APPLICATION NUMBER: 60/089952
PRIOR APPLICATION NUMBER: 60/090254
PRIOR APPLICATION NUMBER: 60/090349
PRIOR APPLICATION NUMBER: 60/090349
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PRIOR APPLICATION NUMBER: 60/090432
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PRIOR APPLICATION NUMBER: 60/090433
PRIOR APPLICATION NUMBER: 60/090434
PRIOR PRILING DATE: 1998-06-24
PRIOR APPLICATION NUMBER: 60/090445
PRIOR APPLICATION NUMBER: 60/090454
PRIOR APPLICATION NUMBER: 60/090454
PRIOR APPLICATION NUMBER: 60/090472
PRIOR APPLICATION NUMBER: 60/090472
PRIOR PRILING DATE: 1998-06-24
PRIOR APPLICATION NUMBER: 60/090472
PRIOR PRILING DATE: 1998-06-24
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1998-07-01 NUMBER: 60/ 1998-07-02 NUMBER: 60/ 1998-07-02 NUMBER: 60/ 1998-07-02 NUMBER: 60/ 1998-07-07 NUMBER: 60/ NUMBER: 60/	1998-06-22 NUMBER: 60, 1998-06-22 NUMBER: 60, 1998-06-22 NUMBER: 60, 1998-06-22 NUMBER: 60, 1998-06-22 NUMBER: 60, 1998-06-22 NUMBER: 60, 1998-06-22 NUMBER: 60, 1998-06-26 NUMBER: 60, 1998-06-26 NUMBER: 60, 1998-06-26 NUMBER: 60, 1998-06-26 NUMBER: 60, 1998-06-26 NUMBER: 60, 1998-07-00, 1998-07-00, 1998-07-00, 1998-07-00,	1998-0 NUMBER:	NUMBER: 60 1998-06-1 1998-06-1 1998-06-1 1998-06-1 NUMBER: 60 1998-06-1 NUMBER: 60 1998-06-1 NUMBER: 60 1998-06-1 NUMBER: 60 1998-06-1 1998-06-2 NUMBER: 60 1998-06-2 NUMBER: 60 1998-06-2 NUMBER: 60
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OR FILING DATE: 1998-05-28
OR APPLICATION NUMBER: 60/087607
OR FILING DATE: 1998-06-02
OR APPLICATION NUMBER: 60/087609
OR FILING DATE: 1998-06-02
OR FILING DATE: 1998-06-02
OR FILING DATE: 1998-06-03
OR FILING DATE: 1998-06-04
OR APPLICATION NUMBER: 60/088025
OR FILING DATE: 1998-06-04
OR APPLICATION NUMBER: 60/088026
OR FILING DATE: 1998-06-04
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OR FILING DATE: 1998-06-04
OR APPLICATION NUMBER: 60/088028
OR FILING DATE: 1998-06-04
OR APPLICATION NUMBER: 60/088030
OR FILING DATE: 1998-06-05
OR APPLICATION NUMBER: 60/08826
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OR APPLICATION NUMBER: 60/088217
OR APPLICATION NUMBER: 60/088210
OR APPLICATION NUMBER: 60/089512
OR APPLICATION NUMBER: 60/089512
OR APPLICATION NUMBER: 60/089520
OR APPLICATION N

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APPLICANT: Tumas, Daniel
APPLICANT: Watanabe, Colin K.
APPLICANT: Williams, P. Mickey
APPLICANT: Zhang, Zemin I.
APPLICANT: Zhang, Zemin I.
APPLICANT: Wood, William I.
APPLICANT: Zhang, Zemin I.
APPLICANT: Nood, William I.
APPLICANT: Nood, William I.
APPLICATION III Secreted and Transmembrane Polypeptides and Nucleic Title Of INVENTION.
CURRENT APPLICATION NUMBER: U$709/989,732
CURRENT FILING DATE: 2001-11-19
PRIOR APPLICATION NUMBER: 60/062250
PRIOR APPLICATION NUMBER: 60/065186
PRIOR APPLICATION NUMBER: 60/065186
PRIOR FILING DATE: 1997-10-17
PRIOR APPLICATION NUMBER: 60/065311
PRIOR APPLICATION NUMBER: 60/065311
PRIOR APPLICATION NUMBER: 60/06570
PRIOR APPLICATION NUMBER: 60/07945
PRIOR APPLICATION NUMBER: 60/07945
PRIOR APPLICATION NUMBER: 60/07945
PRIOR APPLICATION NUMBER: 60/07940
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PRIOR APPLICATION NUMBER: 60/084600
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PRIOR APPLICATION NUMBER: 60/084600
PRIOR FILING DATE: 1998-05-28
PRIOR PILING DATE: 1998-05-28
PRIOR APPLICATION NUMBER: 60/08706
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US-09-989-732-407
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PRIOR APPLICATION NUMBER: 60/092182
PRIOR FILING DATE: 1998-07-09
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Gerritsen, Mary E.
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Gurney, Austin L.
Kljavin Turr
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20020123463A1
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                                 PRIOR APPLICATION NUMBER: 60/087609
PRIOR FILLING DATE: 1998-06-02
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PRIOR FILLING DATE: 1998-06-03
PRIOR FILLING DATE: 1998-06-04
PRIOR PAPLICATION NUMBER: 60/088021
PRIOR APPLICATION NUMBER: 60/088025
PRIOR APPLICATION NUMBER: 60/088026
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PRIOR APPLICATION NUMBER: 60/088026
PRIOR PRILING DATE: 1998-06-04
PRIOR PRILING DATE: 1998-06-05
PRIOR PRILING DATE: 1998-06-10
PRIOR PRILING DATE: 1998-06-11
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PRIOR PRILING DATE: 1998-06-12
PRIOR PRILING DATE: 1998-06-15
PRIOR PRILING DATE: 1998-06-16
PRIOR PRILING DATE: 1998-06-17
PRIOR PRILING DATE: 1998-06-17
PRIOR PRILING DATE: 1998-06
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NUMBER: 60: 1998-06-1998-06-18

80/089908

DR PELLING DATE: 1998-06-19
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BR FILLING DATE: 1998-06-19
BR APPLICATION NUMBER: 60/08
BR FILLING DATE: 1998-06-22
BR FILLING DATE: 1998-06-23
BR FILLING DATE: 1998-06-23
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BR FILLING DATE: 1998-06-23
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60/090254 60/090252

60/090540 60/090542

60/090535 60/090472 60/090445 60/090444 60/090435 60/090431 60/090429 60/090355

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APPLICANT: Tumas, Daniel
APPLICANT: Williams, P. Mickey
APPLICANT: Williams, P. Mickey
APPLICANT: Williams, P. Mickey
APPLICANT: Williams, P. Mickey
APPLICANT: Zhang, Zemin
ITILE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
ITILE OF INVENTION: Secreted and Transmembrane Polypeptides
ITILE OF INVENTION NUMBER: US/09/991,073
ITILE OF INVENTION NUMBER: 60/049787
ITILE OF I
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US-09-991-073-407
; Sequence 407, Application US/09991073
; Sequence 407, Application US/09991073
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Best Local S
Matches 78
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Godowski, Paul J.
Grimaldi, J.Christopher
Gurney, Austin L.
Kljavin, Ivar J.
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Baker, Kevin P.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Baker, Kevin P.
Botstein, David
Desnoyers, Luc
Eaton, Dan L.
Ferrara, Napoleone
Fong, Sherman
Gerber, Hanspeter
Gerritsen, Mary E.
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Roy, Margaret Ann
Stewart, Timothy A.
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Pan, James
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lo. 1.9e-08;
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OR APPLICATION NUMBER: 60,709057
OR FILING DATE: 1998-06-24
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OR APPLICATION NUMBER: 60,7090678
OR FILING DATE: 1998-06-25
OR APPLICATION NUMBER: 60,7090690
OR FILING DATE: 1998-06-25
OR APPLICATION NUMBER: 60,7090694
OR FILING DATE: 1998-06-25
OR APPLICATION NUMBER: 60,7090695
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OR APPLICATION NUMBER: 60,709155
OR FILING DATE: 1998-07-02
OR APPLICATION NUMBER: 60,7091626
OR FILING DATE: 1998-07-02
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Ouery Match 14.2%; Score 78; DB 10; Length 570; Best Local Similarity 100.0%; Pred. No. 1.9e-08;

PRIOR APPLICATION NUMBER: 60/08322 PRIOR EILING DATE: 1998-04-28 PRIOR APPLICATION NUMBER: 60/084600 PRIOR FILING DATE: 1998-05-07 PRIOR APPLICATION NUMBER: 60/087106 PRIOR APPLICATION NUMBER: 60/087106 PRIOR APPLICATION NUMBER: 60/087607 PRIOR FILING DATE: 1998-06-02 PRIOR FILING DATE: 1998-06-02 PRIOR FILING DATE: 1998-06-02 PRIOR FILING DATE: 1998-06-02 PRIOR APPLICATION NUMBER: 60/087759 PRIOR APPLICATION NUMBER: 60/087827 PRIOR APPLICATION NUMBER: 60/087827 PRIOR FILING DATE: 1998-06-02 PRIOR FILING DATE: 1998-06-03	REFERENCE: P2730P1C8 REFERENCE: P2730P1C8 REFERENCE: P2730P1C8 REFILING DATE: 2001-11-14 APPLICATION NUMBER: 60/062 FILING DATE: 1997-06-16 APPLICATION NUMBER: 60/062 FILING DATE: 1997-10-17 APPLICATION NUMBER: 60/065 FILING DATE: 1997-11-12 APPLICATION NUMBER: 60/065 FILING DATE: 1997-11-13 APPLICATION NUMBER: 60/065 FILING DATE: 1997-11-24 APPLICATION NUMBER: 60/078 FILING DATE: 1997-11-24 APPLICATION NUMBER: 60/078 FILING DATE: 1998-02-25 APPLICATION NUMBER: 60/078 APPLICATION NUMBER: 60/078 APPLICATION NUMBER: 60/078 APPLICATION NUMBER: 60/078	APPLICANT: Eaton, Dan L. APPLICANT: Forgram, Napoleone APPLICANT Forg, Sherman APPLICANT Gerber, Hanspeter APPLICANT Gerber, Hanspeter APPLICANT Gerber, Mary E APPLICANT Gerber, Mary E APPLICANT Goddward, Audrey APPLICANT Goddward, Audrey APPLICANT Grimaldi, J. Christopher APPLICANT Gurney, Austin L. APPLICANT Hapier, Mary A. APPLICANT Napier, Mary A. APPLICANT Rapier, Mary A. APPLICANT Roy, Margaret Ann APPLICANT Roy, Margaret Ann APPLICANT Tumas, Dahiel APPLICANT Wattnabe, Colin K. APPLICANT Wattnabe, D. Mickey APPLICANT Wood, William I. APPLICANT Wood, William I. APPLICANT Wood, William I. APPLICANT Wood, William I. APPLICANT Statember Bolypeptides and	8; Conservative 0; Mismatches 0; Indels GCAGGGACCGGGTATAAGAAGACCTCGTGCCCTTGCCCGGGCAGCCGCAGGT [
PRIOR FILING DATE: 1998-06-17 PRIOR APPLICATION NUMBER: 60/089600 PRIOR FILING DATE: 1998-06-17 PRIOR APPLICATION NUMBER: 60/08963 PRIOR FILING DATE: 1998-06-17 PRIOR FILING DATE: 1998-06-18 PRIOR PRIOR APPLICATION NUMBER: 60/089907 PRIOR PRIOR PRIOR DATE: 1998-06-18 PRIOR PRIOR FILING DATE: 1998-06-18 PRIOR PRIOR FILING DATE: 1998-06-18 PRIOR PRIOR FILING DATE: 1998-06-18 PRIOR APPLICATION NUMBER: 60/089908 PRIOR PRIOR FILING DATE: 1998-06-18 PRIOR PR		Nucleic	O; PRIOR APPLI 533 PRIOR APPLI 533 PRIOR APPLI 60 PRIOR FILIN 60 PRIOR FILIN 60 PRIOR FILIN 60 PRIOR APPLI 60 PRIOR APPLI 61 PRIOR APPLI 62 PRIOR APPLI 63 PRIOR APPLI 64 PRIOR APPLI 65 PRIOR APPLI 66 PRIOR APPLI 67 PRIOR APPLI 67 PRIOR APPLI 68 PRIOR APPLI 68 PRIOR APPLI 69 PRIOR APPLI 69 PRIOR APPLI 69 PRIOR APPLI 60 PRIOR APPLI 61 PRIOR APPLI 61 PRIOR APPLI 61 PRIOR APPLI

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OR APPLICATION NUMBER: 60/090474
OR APPLICATION NUMBER: 60/090540
OR FILING DATE: 1998-06-24

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DR FILING DATE: 1998-06-24
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OR APPLICATION UNMER: 60/091982
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OR FILING DATE: 1998-07-09 474 GCGAGGACCGGGTATAAGAAGCCTCGTGGCCTTGCCCGGGCAGCCGCAGGTTCCCCGCGC 533 ch 14.2%; So 15 14.2%; So 15 16 17 18; Sonservative 0; Score 78; DB 10; Pred. No. 1.9e-08; 0; Mismatches 0; Length 570; Indels

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TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and
TITLE OF INVENTION: Acids Encoding the Same
FILE REFERENCE: P2730P1C25
FILE REFERENCE: P2730P1C25
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Baker, Kevin P.
Botstein, David
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Godowski, Paul J.
Grimaldi, J. Christopher
Gurney, Austin L.
Kljavin, Ivar J.
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Williams, P. Mickey
Wood, William I.
Zhang, Zemin
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Search completed: September 20, 2003, 03:21:37 Job time: 220.634 secs

Run on: OM nucleic -

Title: Perfect score:

Scoring table: Sequence:

Database

Result No.

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Query Match

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Post-processing: Minimum Match 0%
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score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.
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blood; plasma; serum; ss.
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                           (ABBO ) ABBOTT LAB
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Sequences shown in AAV54616 to AAV54621 represent LU105 specific CC polynucleotide sequences. These are used in the method of the invention CC for detecting target LU105 nucleic acid. The method comprises treating a CC sample with at least one LU105 specific nucleic acid, or its complement CC which is at least 50 percent identical with the LU105 specific nucleic acid sequences (AAV54616 to AAV54621). LU105 is a lung disease marker. CC cells transformed with a recombinant expression system that contains CC LU105 specific nucleic acid fragments, are used to express recombinant CC LU105 specific nucleic acid fragments, are used to express recombinant CC LU105 specific nucleic acid sequences and intibodies are used to detect the LU105 antigen, and correspondingly this antigen is cused to detect specific antibodies, in usual immunoassays The LU105 CC used to detect the LU105 antigen, and correspondingly this antigen, consolitoring, prognosis, prevention, treatment and determination of consolitoring, prognosis, prevention, treatment and determination of customorphisms are also used to screen for specific binding agents, useful therapeutically. LU105 is a marker for lung disease (present at high concentration, in altered form or in an unusual body compartment). LU105 cc can be detected in blood, plasma or serum in an inexpensive, non-invasive
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Query Match
Best Local S
Matches 310
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Billing-medel
Granados EN,
Russell JC, S
   11-MAY-2000
                                                                       AAZ98173 standard;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            New nucleic acid for the lung disease marker LUIO5 - polypeptides, antibodies and genes, used for diagnosis, prevention, treatment of lung disease, specifically cancer
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             (Updated
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les 310; Conservat
                                                                                                                                                                                               301
                                                                                                                                                                                                                                   319
                                                                                                                                                                                                                                                                                                                                       181
                                                                                                                                                                                                                                                                                                                                                                         121 GAGGCCGGGGGGACCTGGCCAACCCCTCGGCACCTCAACCCGCTGAAGCTCCTG
19 GAGGCCGGGGCCGGGACCCTGGCCAACCCCTCGGCACCCTCAACCCCCTGAAGCTCCTG
19 GAGGCCGGGGCCCGGGACCCTGGCCAACCCCTCGGCACCCTCAACCCCTTGAAGCTCCTG
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                                                                                                                                                           ACAGTGTTTGGC 312
                                                                                                                                                                                                                                                                                                                               CTGAGCAGCCTGGGCATCCCCGTGAACCACCTCATAGAGGGCTCCCAGAAGTGTGTGGCT
                                                                                                                                                                                                                                                                                                                                                                                                                                            ATGAAGCTCGCCGCCCTCCTGGGGCTCTGCGTGGCCCTGTCCTGCAGCTCCGCTCGTGCT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     519 BP; 78 A; 190 C; 170 G; 81 T; 0 other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             on
                                                                                                                                                                                                                                     GAGCTGGGTCCCCAGGCCGTGGGGGGCCGTGAAGGCCCTGAAGGCCCTGCTGGGGGGCCCCTG
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Hodges SC,
Stroupe SD;
   (first
                                                                       CDNA;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      0;
                                                                         ВP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Score 308.8; DB 1
Pred. No. 4.5e-53;
0; Mismatches 2
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ATGAAGCTCGCCGCCCTCCTGGGGCTCTGCGTGGCCCTGTGCAGCTCCGCTCGTGCT 60

Query Match Best Local S Matches 310

al Similarity 310; Conserv

99.0%; llarity 99.4%; Conservative

Pred. No. 4.5e. 0; Mismatches

; ;.5e-53; 2;

Indels Length

0;

Gaps

0;

Sequence

543

BP;

89 A; 194 C;

178 G; 82 T;

0 other; DВ 21;

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CC harding cancer), inflammation, cardiovascular, neurological, concluding cantivorsis, acquired immune deficiency soft disease, microbial, neurological, concluding cantivorsis, hepatotropic, acquired inmune deficiency syndrome, anaemia, crischaemic heart disease, microbial or other infections, congestive or ischaemic heart disease, microbial or other infections, congestive or clischaemic heart disease, microbial or other infections, congestive or clischaemic heart disease, Alahelmer's, parkinson's or Huntington's conscience, heart disease, Alahelmer's, parkinson's or Huntington's concletic acids can be used for the recombinant production of HSPP, for detecting HSPP in standard hybridisation and amplification assays (for concletic acids can be used for the recombinant production of HSPP, for detecting the production, and for chromosomal mapping. HSPP are also used to cantagonists (potential therapeutic appendix, habere used to diagnose, or cantagonists potential therapeutic agents). Ab are used to diagnose, or cantagonists, in competitive drug screens, and for purification of HSPP creative drug screens, and for purification of H
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      26-JUN-1998;
31-JUL-1998;
01-OCT-1998;
11-DEC-1998;
                                            antagonists, from natural
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               New human signal peptide-containing proteins useful in treatment, prevention and diagnosis of e.g. cancer, inflammation and cardiovascular disease
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Lal P, 7
Akerblom
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Human; signal peptide-containing protein; HSPP; diagnosis; cancer; inflammation; cardiovascular disease; anticancer; anti-inflammatory; antimicrobial; nootropic; neuroprotective; cardiovascular; hepatotropic; antiasthmatic; gene therapy; cell proliferation; neurological disorder; reproductive disorder; developmental disorder; arteriosclerosis; cirrhosis; psoriasis; acquired immune deficiency syndrome; anaemia; asthma; Crohn's disease; infection; Alzheimer's disease; schizophrenia; parkinson's disease; Huntington's disease; ovulatory defect; markinson's disease; Huntington's disease; ovulatory defect;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          06-JAN-2000
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            (INCY-) INCYTE PHARM INC
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DB; AAY87288.
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om IE,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Page 289; 327pp; English.
                                               sources
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98US-0094983.
98US-0102686.
98US-0112129.
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Young J, Yue
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     CDNA
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Query Match
                                                                           The present sequence is a lung specific gene (LSG) Lng107 from human clone ID 586271. The LSG has high level of tissue specificity for lungs and is overexpressed in cancerous tissues. The sequence serves as a diagnostic marker for detecting, monitoring, staging and prognosticating lung cancer. The diagnosis involves comparing levels of LSG in samples obtained from patient and normal control.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  AAZ29723 standard; DNA; 543
                                                                                                                                                                                                                                                                                                                                                                                    Yang F,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Human lung specific gene Lng107.
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                                          Sequence
                                                                                                                                                                                                                                       Claim 6;
                                                                                                                                                                                                                                                                           A new method for diagnosing, monitoring and staging lung cancer
                                                                                                                                                                                                                                                                                                                             P-PSDB;
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                                          543 BP;
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                                                                                                                                                                                                                                                                                                                                                                                    Macina RA,
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                                        89 A; 194 C; 178 G; 82 T;
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21;
Length 543;
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                                                        WPI; 199
P-PSDB;
                                                                                 Billing-medel PA, Cohen M, Colpitts Granados EN, Hodges SC, Klass MR, I Russell JC, Stroupe SD;
                                                                                                                                                                                                                                                                           LU105;
blood;
                     New nucleic acid for the lung disease marker LU105 - polypeptides, antibodies and genes, used for diagnosis, prevention, treatment of lung disease, specifically cancer
                                                                                                                                                                                                                                                                                                                    25-MAR-2003
30-OCT-1998
        Claim 11; Fig
                                                                                                                   (ABBO ) ABBOTT
                                                                                                                                     31-JAN-1997;
                                                                                                                                                     30-JAN-1998;
                                                                                                                                                                       06-AUG-1998.
                                                                                                                                                                                       WO9833926-A1
                                                                                                                                                                                                                                                           Homo
                                                                                                                                                                                                                                                                                                   LU105 specific consensus polynucleotide sequence.
                                                                                                                                                                                                                                                                                                                                              AAV54620;
                                                                                                                                                                                                                                                                                                                                                               AAV54620 standard; cDNA; 562
                                                          1998-437479/37.
DB; AAW75868.
                                                                                                                                                                                                                                                           sapiens
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              213
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        121 GAGGCCGGGGCCCGGGACCCCTGGCCAACCCCTCAACCCGCTGAAGCTCCTG
                                                                                                                                                                                                                                                                                                                                                                                                          393
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              lung disease marker; plasma; serum; ss.
                                                                                                                                                                                                                                                                                                                                                                                                        CTGAGCAGCCTGGGCATCCCCGTGAACCACCTCATAGAGGGCTCCCCAGAACTGTGTGGCCT
                                                                                                                                                                                                                                                                                                                                                                                                                                        GAGGCCGGGGCCGGGACCCTGGCCAACCCCCTCGGCACCCTCAACCCCGCTGAAGCTCCTG
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                                                                                                                                                                                                                                                                                                                    (updated)
        1; 123pp; English
                                                                                                                   LAB.
                                                                                                                                     97US-0791710
                                                                                                                                                      98WO-US01766
                                                                                                                                                                                                                                Location/Qualifiers 122..436
                                                                                                                                                                                                      /transl_except= (pos:176..178, aa:Val) .
/product= "LU105 polypeptide"
                                                                                                                                                                                                                                                                                                                     entry)
                                                                                                                                                                                                                                                                                                                                                                                                                         312
                                                                                                                                                                                                                                                                                                                                                                                                          404
                                                                                                                                                                                                                                                                                   immunoassay; lung disease; cancer;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Pred. No. 4.5e-53;
0; Mismatches 2;
                                                                                                                                                                                                                                                                                                                                                               BP.
                                                                                          % TL, Friedman PN, Gordon J;
Kratochvil JD, Robertsrapp L;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Indels
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RESULT 5
ABK4 0267
ID ABK4
AC ABK4
AC ABK4
DT 15-C
XX CDNI
XX Hum
KW Hum
KW Heul
KW Jeel
KW gen
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XX Hom
XX Hom
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             γQ
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Best Local S
Matches 310
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                                                                                                                                                                                      Human; PRO; benign tumour; malignant tumour; lymphoid malignancy; leukaemia; neuronal disorder; stromal disorder; blastocoelic disorder; inflammatory disorder; immune disorder; angiogenic disorder; gene therapy; cytostatic; neuroprotective; gene; ss.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ABK40267 standard;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     (Updated on 25-MAR-2003 to correct PI field.)
                                                                                                                                                                                                                                                                                                                             cDNA encoding human
                                                                                                                                                                                                                                                                                                                                                                                  15-JUL-2002
                                                                                                                                                                                                                                                                                                                                                                                                                                       ABK40267;
                                                                                    WO200153486-A1
                                                                                                                                          Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              310;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ATGAAGCTCGCCÓCCCTCCTGGGGCTCTGCGTGGCCCTGTCCTGCAGCTCCGCTCCT 60
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  GAGCTGGGTCCCCAGGCCGTGGGGGCCCTGAAGGCCCTGAAGGCCCTGCTGGGGGCCCTG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             CTGAGCAGCCTGÓGCATCCCCGTGAACCACCTCATAGAGGGCTCCCAGAAGTGTGTGGCT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TTCTTAGTGGGCTCGGCCAAGCCTGTGGCCCAGCCTGTCGCTGCGCTGGAGTCGGCGGCG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    GAGGCCGGGGCCGGGACCCTGGCCAACCCCTCAACCCCTCAACCCCTGAAGCTCCTG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       GAGGCCGGGGCCGGGACCCTGGCCAACCCCCTCGGCACCCTCAACCCGCTGAAGCTCCTG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TTCTTAGTGGGCTCGGCCAAGCCTGTGGCCCAGCCTGTCGCCTGGAGTCGGCGCG
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llarity 99.4%;
Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             CDNA; 569
                                                                                                                                                                                                                                                                                                                         PRO1245 polypeptide.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Score 308.8; DB 19;
Pred. No. 4.5e-53;
0; Mismatches 2;
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Best Local Similarity 99.4
Matches 310; Conservative
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20-JUL 1999
26-JUL 1999
26-JUL 1999
28-JUL 1999
17-AUG 1999
31-AUG 1999
31-AUG 1999
31-NOV 1999
30-NOV 1999
01-BEC 1999
01-DEC 1999
01-DEC 1999
05-JAN 2000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          08-MAR-1999;
11-MAR-1999;
11-MAY-1999;
02-JUN-1999;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Ashkenazi AJ,
Marsters SA,
Watanabe CK,
                                                                                                                                                                                                                                                                                      The present invention relates to the isolation of novel human PRO polypeptides and the polynuclectide sequences encoding them. The PRO polypeptides, agonists, antagonists or anti-PRO antibodies are useful for treating benign or malignant tumours (e.g. renal, kidney, bladder, breast, etc), leukaemias and lymphoid malignancies, other disorders such as neuronal, glaal, astrocytal, hypothalamic, glandula macrophagal, stromal and blastocoelic disorders, inflammatory, immune and angiogenic disorders. The polynucleotide sequences are also useful in gene therapy. ABK40254-ABK40288 encode for the human PRO polypeptides of the invention.
                                                                                                                                                                                                                                                                                                                                                                                                                                   Thirty five nucleic acids encoding PRO polypeptides, useful for treating benign or malignant tumours, leukaemias and lymphoid malignancies, inflammatory, angiogenic and immunologic disorders
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  11-FEB-2000;
                                                                                                                                                                                                                                                                                                                                                                                                               Claim 50; Fig 27; 302pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          (GETH ) GENENTECH INC.
                                                                                                                                                                                                                                                                     Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                P-PSDB;
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DB; AAU86141.
319
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                                          TTCTTAGTGGGCTCGGCCAAGCCTGTGGCCCAGCCTGTCGCTGCGCTGGAGTCGGCGCG
                                                                                                                                                                             569 BP; 128 A; 190 C; 170 G; 81 T; 0 other;
             GAGCTGGGTCCCCAGGCCGTGGGGGCCCTGAAAGGCCCTGAAGGCCCTGCTGGGGGGCCCTG
GAGCTGGGTCCCCAGGCCGTGGGGGCCCTGAAGGCCCTGAAGGCCCTGCTGGGGGCCCTG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       99WO-US12252
99WS-140650P
99US-140653P
99US-144758P
99US-14652P
99US-14622P
99US-14622P
99US-151689P
99US-151689P
99WO-US20111
99WO-US20111
99WO-US20313
199WO-US28313
99WO-US28313
99WO-US28313
99WO-US28313
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Pan J, Pitti RM,
Wood WI;
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i RM, Roy MA,
                                                                                                                                                                                                                         0;
                                                                                                                                                                                                                                     Score 308.8; DB Pred. No. 4.5e-53
                                                                                                                                                                                                                           Mismatches
                                                                                                                                                                                                                                                24; Length
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Stone DM;
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RESULT																						
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19-JUN-1998; 98US-0090; 22-JUN-1998; 98US-0090; 22-JUN-1998; 98US-0090; 23-JUN-1998; 98US-0090; 24-JUN-1998; 98US-0090; 25-JUN-1998; 98US-0091; 25-JUN-1998; 98US-0095; 25-JUN-1998; 25-JUN-1998; 25-JUN-1998; 25-JUN-1998; 25	98US-0089599. 98US-0089600. 98US-0089601. 98US-0089901. 98US-0089901. 98US-0089904.	98US-0089512. 98US-0089514. 98US-0089532. 98US-0089538.	98US-0088876. 98US-0089090. 98US-0089105. 98US-0089440.	98US-0088826. 98US-0088826. 98US-0088858. 98US-0088863.	98US-0088742. 98US-0088810. 98US-0088811. 98US-0088824.	98US-0088740. 98US-0088741.	98US-0088722. 98US-0088722.	98US-0088217.	98US-0088326. 98US-0088167.	98US-0088029. 98US-0088030. 98US-0088033	98US-0088025. 98US-0088025.	98US - 0087827.	98US-0087607.	225			<pre>polypeptide; PRO polypeptide; LDL receptor; TIE ; receptor immunoadhesin; gene mapping; ss.</pre>	protein PRO1245 encoding	first		cDNA; 570	
19-JUN-1998; 98US-0090; 22-JUN-1998; 98US-0090; 22-JUN-1998; 98US-0090; 23-JUN-1998; 98US-0090; 24-JUN-1998; 98US-0090; 25-JUN-1998; 98US-0091; 25-JUN-1998; 98US-0095; 25-JUN-1998; 25-JUN-1998; 25-JUN-1998; 25-JUN-1998; 25	מק ק ק ק ק ק ק ק ק ק ק ק ק ק ק ק ק ק ק	אס אס אס אס אס	מי קים קים קים	אס אס אס	אם אם אם	א מי	אק אק	אק אק	מי הים הים	אפ	ਸ਼ਕ	אים אים	יים תקי	הים הים	יים מים	הים הים	ים מים מים	ים פי נ	יי סי נו ג'יר ו	היים היים	אם הם	יי ט ט ט ט ט ט ט ט ט ט ט ט ט ט ט ט ט ט
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Query Match
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Matches 310
                                                                                                                                                                                                                                                                                                         The invention provides membrane-bound PRO polypeptides and polynucleotides encoding them. The PRO sequences of the invention were identified based on extracellular domain homology screening. The PRO sequences have homology with proteins including LDL receptors, TIE ligands and various enzymes. The membrane-bound proteins and receptor molecules are useful as pharmaceutical and diagnostic agents. Receptor immunoadhesins, for instance, can be used as therapeutic agents to block receptor-ligand interactions. The membrane-bound proteins can also be employed for screening of potential peptide or small molecule inhibitors of the relevant receptor/ligand interaction. The PRO encoding sequences are useful as hybridization probes, in chromosome and gene mapping and in the generation of antisense RNA and DNA. PRO nucleic acid sequences will also be useful for the preparation of PRO polypeptides, especially by recombinant techniques.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                20 - AUG - 1998
24 - AUG - 1998
26 - AUG - 1998
27 - AUG - 1998
28 - AUG - 1998
29 - AUG - 1998
20 - AUG - 1998
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Wood V
                                                                                                                                                                                                                                                                                           Sequence
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B; AAY66757.
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                                                                                                                       ATGAAGCTCGCCGCCCTCCTGGGGCTCTGCGTGCCCTGTGCAGCTCCGCTCGTGCT
                                                                               CTGAGCAGCCTGGGCATCCCCGTGAACCACCTCATAGAGGGCTCCCAGAAGTGTGTGGCT
                                                  GAGCTGGGTCCCCAGGCCGTGGGGGCCCTGAAGGCCCTGAAGGCCCTGCTGCGGGGCCCTG
                                                                                                                                                                                                                                                                                           570 BP; 129
ACAGTGTTTGGC
            ACAGTGTTTGGC
                                         GAGCTGGGTCCCCAGGCCGTGGGGGCCCTGAAGGCCCCTGCTGGGGGCCCCTG
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Yuan
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98US-009751
98US-0097951
98US-0097952
98US-0097952
98US-0097975
98US-0097971
98US-0097971
98US-0097978
98US-0097978
98US-0097979
98US-0098014
98US-0098014
98US-0098555
98US-0115565
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                   312
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        and related nucleotide
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                                                                                                                                                                                                                                                   0;
                                                                                                                                                                                                                                                 Score 308.8; 1 Pred. No. 4.5e 0; Mismatches
                                                                                                                                                                                                                                                                                            C; 170
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                                                                                                                                                                                                                                                                                           G;
                                                                                                                                                                                                                                                                                         81 T; 0 other;
                                                                                                                                                                                                                                                            ; DB 21;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Smith V,
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23-JUN-1999
23-JUN-1999
07-JUL-1999
26-JUL-1999
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17-AUG-1999
17-AUG-1999
15-SEP-1999
15-SEP-1999
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16-DEC-1999
16-DEC
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99US-0144758
99US-0145698
99US-014522
99US-0149396
99WO-US21190
99WO-US211547
99US-015863
99WO-US23091
99WO-US30095
99WO-US3001
99WO-US3001
2000WO-US0021
2000WO-US0021
2000WO-US00376
2000WO-US04341
2000WO-US04341
2000WO-US05804
2000WO-US05804
2000WO-US05884
2000WO-US05884
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          99WO-US12252
99US-0141037
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Ashkenazi AJ, Baker KP, Botstein D, Desnoyers L, Eaton Ferrara N, Fong S, Gerber H, Gerritsen ME, Goddard A, Grimaldi CJ, Gurney AL, Kljavin IJ, Napier MA, Pan J, Roy MA, Stewart TA, Tumas D, Watanabe CK, Williams PM, DL; Godowski Paoni NF; Wood WI; рJ;

WPI; 2001-032160/04. P-PSDB; AAB65280.

PRO polynucleotides used bioactive molecules such specific cells, to cause to produce polypeptides used to target as toxins, radiolabels or antibodies, to targeted cell death -

Claim 2; Fig 289; 935pp; English.

The present invention describes human secreted and transmembrane PRO proteins. The PRO proteins have cytostatic activity. The PRO proteins can be used for targeted delivery of bloactive molecules, such as toxins, radiolabels or antibodies, that cause cell death. PRO nucleotide sequences, and their fragments, can be used as hybridisation probes, in chromosomal and gene mapping, and in the generation of anti-sense RNA and DNA. They may also be used to produce transgenic animals which are used to develop and screen therapeutically useful reagents. The PRO

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RESULTA
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ABX803
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Best Local S
Matches 310
   05-NOV-1997;
16-SEP-1998;
17-SEP-1998;
07-OCT-1998;
01-DEC-1998;
05-JAN-1999;
                                                                                                                                                                                                                                                                                                                                                                                                       Human; PRO; hypertrophy of neonatal heart; angiogenesis; wound healing; cardiac insufficiency disorder; cancer; tumour; immune response; adrenal cortical capillary endothelial growth; c-fos induction; vascular endothelial growth factor inhibition; VEGF inhibition; endothelial cell growth inhibitor; T-lymphocytes stimulation; retinal neurons cell survival; rod photoreceptor cell survival; rod photoreceptor cell survival; retinal disorder; retinitis pigmentosum; kidney disorder; mammallian kidney mesangial cell proliferation; Berger disease; denondrocyte proliferation; cohondrocyte redifferentiation; sports injury; arthritis; gene; ds.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    nucleotide and protein sequence can be used for tissue typing and in treating cancer. Anti-PRO antibodies can be used in diagnostic assays. AAF44270 to AAF44470 represent PCR primers and hybridisation probes us in the isolation of human PRO sequences. AAF44087 to AAF44269 and AAB65154 to AAB65300 represent human PRO polynuclotide and protein sequences given in the exemplification of the present invention.
                                                                                                                                                                                        14-NOV-2001;
                                                                                                                                                                                                                                                  19-SEP-2002
                                                                                                                                                                                                                                                                                                    US2002132252-A1.
                                                                                                                                                                                                                                                                                                                                                              Ното
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Similarity 99.4%;
10; Conservative (
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                                                                                                                                                                                               2001US-0990442
97WO-US20069.
98WO-US19437.
98WO-US21141.
98WO-US251141.
98WO-US25108.
99WO-US00106.
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08-MAR-1999
15-SEP-1999
30-NOV-1999
30-NAR-2000
30-MAR-2000
30-MAR-2000
30-MAR-2000
30-MAR-2000
30-MAR-2000
30-MAR-2000
30-MAR-2000
30-MAR-2000
30-MAR-2000
30-MAR-1998
30-JUN-2001
31-AUG-2000
30-MAR-1998
30-JUN-1998
99WO-US12528
99WO-US12528
99WO-US21252
99WO-US213137
99WO-US28301
99WO-US28301
99WO-US20301
99WO-US20301
99WO-US20301
99WO-US20301
99WO-US20301
99WO-US20301
2000WO-US2031
2000WO-US204414
2000WO-US204414
2000WO-US20504
2000WO-US20504
2000WO-US20504
2000WO-US20504
2000WO-US20504
2000WO-US20504
2000WO-US20501
2000WO-US2050
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Mon

240

198 180 258

318

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CC The invention describes an isolated human PRO polypeptide. The PRO CC polypeptides are useful in detecting PRO polypeptides in a sample, in CC linking a bioactive molecule to a cell expressing a PRO polypeptide, and CC in modulating at least one biological activity of a cell expressing a PRO CC polypeptide. PRO1312 stimulates hypertrophy of neonatal heart and is thus CC useful for treating cardiac insufficiency disorders. PRO1134 and PRO186 CC stimulate adrenal cortical capillary endothelial growth, and PRO186 CC PRO1360 and PRO187 induce c-fos in endothelial growth, and PRO186 CC PRO1360 and PRO187 induce c-fos in endothelial cells, and are thus useful for treating cancerous tumours. PRO812 inhibits vascular CC endothelial growth factor (VEGF) stimulated proliferation of endothelial cells and is thus useful for inhibiting endothelial cell growth. PRO826, PRO186, PRO186, PRO186, PRO186, PRO186, PRO186, PRO186, PRO187 stimulated proliferation of endothelial cell growth in CC mammals which would be beneficial in inhibiting tumour growth. PRO826, CC pro1068, PRO186, PRO1375 stimulated proliferation of condinated Tymphocytes and are therapeutically useful for enhancing condinated proliferation of mammaliane kidney disorders of injuries, PRO826, PRO188 or PRO132 enhances survival/proliferation of condisorders of injuries, PRO826, PRO188 or PRO132 enhances survival/proliferation of mammaliane kidney mesangial cells, and therefore are useful for treating sports injuries, and are thus useful for treating cells cells, and therefore are useful for treating sports injuries, and are therapeutical and kidney mesangial cells, and therefore are useful for treating sports injuries, and are therapeutical and kidney mesangial cells, and therefore are useful for treating sports injuries, and arthritis. This sequence represents a novel human PRO protein polynucleotide.
      B 8
                                                          Query Match
Best Local Similarity
Matches 310; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     12-JUN-1998
16-JUN-1998
16-JUN-1998
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Ferrara N,
Grimaldi J
Roy MA, S
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         WPI; 200
P-PSDB;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Novel isolated PRO polypeptides e.g., PRO826, PRO1068, PRO1184, PRO1346 and PRO1375, which stimulate proliferation of stimulated T-lymphocytes are therapeutically useful for enhancing immune response and in cancer
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Zhang
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Claim
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           treatments
                                                                                                               Sequence
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DB; ABU59174.
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                                                                                                               570
    ATGAAGCTCGCCGCCCTCCTGGGGCTCTGCGTGGCCCTGTCCTGCAGCTCCGCTGCT 60
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98US-089440P

98US-089514P

98US-089532P

98US-089538P

98US-089598P

98US-089598P

98US-089508P

98US-089603P

98US-089603P

98US-089603P

98US-08907P

98US-089908P

98US-089908P
                                                        99.0%;
ilarity 99.4%;
Conservative
                                                                                                             BP; 129
                                                                                                               A; 190 C; 170 G; 81 T; 0 other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                English.
                                                        Score 308.8; DB 25; Length Pred. No. 4.5e-53; O; Mismatches 2; Indels
                                                                                      570;
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Godowski
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RESULT 9
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16-SEP-1997;
17-SEP-1998;
07-OCT-1998;
01-DEC-1998;
05-JAN-1999;
05-JAN-1999;
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07-OCT-1999;
07-OCT-1999;
07-DEC-1999;
07-DE
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ABX80890 standard;
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Best Local Similarity 99.4%;
Matches 310; Conservative
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22-DEC-1998;
12-MAR-1999;
23-JUN-1999;
05-NOV-1997;
16-SEP-1998;
17-SEP-1998;
07-OCT 1998;
01-DEC-1998;
05-JAN 1999;
08-MAR-1999;
02-JUN-1999;
15-SEP-1999;
15-SEP-1999;
                                                                                                                                                                                                                                                                                                           Human; PRO; hypertrophy of neonatal heart; angiogenesis; wound healing cardiac insufficiency disorder; cancer; tumour; immune response; adrenal cortical capillary endothelial growth; c-fos induction; vascular endothelial growth factor inhibition; VEGF inhibition; endothelial cell growth inhibitor; T-lymphocytes stimulation; retinal neurons cell survival; rod photoreceptor cell survival; rod photoreceptor cell survival; rad photoreceptor cell survival; mammalian kidney mesangial cell proliferation; Berger disease; denondrocyte proliferation; sports injury; arthritis; gene; ds.
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98US-113296P.
99US-123957P.
99US-141037P.
   97WO-US20069.
98WO-US19330.
98WO-US19437.
98WO-US21141.
98WO-US25108.
99WO-US0106.
99WO-US0108.
99WO-US1252.
99WO-US1252.
99WO-US1254.
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Pred. No. 4.5e-53;
0; Mismatches 2;
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         30-NOV-1999
01-DEC-1999
101-DEC-1999
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101-DEC-1999
101-DEC-1999
201-DEC-1999
201-DEC-1999
101-DEC-1999
102-MAR-2000
11-FEB-2000
11-FEB-2000
11-MAR-2000
11-MAR-1998
11-JUN-1998
10-JUN-1998
11-JUN-1998
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99WO-US283313

99WO-US283631

2000WO-US300219

2000WO-US300219

2000WO-US00376

2000WO-US054414

2000WO-US05841

2000WO-US05841
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RESULT 11
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Best Local Similarity 99.4%;
Matches 310; Conservative
05-NOV-1997;
16-SEP-1998;
17-SEP-1998;
07-OCT-1998;
01-DEC-1998;
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18-AUG-1998
18-AUG-1998
18-AUG-1998
19-AUG-1998
19-AUG-1998
20-AUG-1998
26-AUG-1998
                                                                                                                                                                        14-NOV-2001;
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                                                                                                                                                                                                                                                                                                                                                                                                   Human; gene; ss; PRO; secreted; transmembrane; signal pharmaceutical; diagnostic; therapeutic; gene therapy
                                                                                                                                                                                                                                 31-OCT-2002
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Human
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    01-MAY-2003 (first
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ABX90363;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              secreted/transmembrane protein cDNA, #163.
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Ashkenazi AJ, Baker KP, Botstein D, Desnoyers L, Eaton Ferzara N, Fong S, Gerber H, Gerritsen ME, Goddard A, Grimaldi JC, Gurney AL, Kljavin IJ, Napier MA, Pan J, Roy MA, Stewart TA, Tumas D, Watanabe CK, Williams PM, Zhang Z; 1 DL; Godowski PJ; Paoni NF; 1, Wood WI;

WPI; 2003-288106/28. P-PSDB; ABU60604.

New transmembrane polypeptides and nucleic acids encoding the polypeptides, useful in gene therapy, in chromosome identification, chromosome markers, or in generating probes as

Claim 2 Fig 289; 650pp; English.

The invention discloses isolated PRO secreted/transmembrane polypeptides CC comprising a sequence without signal peptide and the nucleic acid cencoding them. The polypeptides can be used to raise antibodies that CC specifically bind to the PRO polypeptide, for linking a bioactive combination of the properties and properties and for modulating at least CC one biological activity of a cell. The PRO polypeptides or polynucleotides are also useful in gene therapy, in chromosome cc identification, as chromosome markers, or in generating probes. The PRO polypeptides are useful as molecular markers for protein cell-critication, as the isolated nucleic acids may be used for cecombinantly expressing those markers. The PRO polypeptides are useful cardismay also be used in tissue typing. Anti-PRO antibodies are useful in diagnostic assays for PRO, and in affinity purification of PRO from CC acids may also be used in tissue typing. Anti-PRO antibodies are useful cardismay also be used in tissue typing. Anti-PRO antibodies are useful and in affinity purification of PRO from CC acids may also assays for PRO, and in affinity purification of PRO from CC acids may also are the genes encoding, the primers amplifying and the CC probes detecting the PRO polypucleotides of the invention.

CC probes detecting the PRO polypucleotides of the invention.

CC format from USPTO at segdata.uspto.gov/sequence.html.

вP; 129 A; 190 C; 170 G; 81 T; 0 other;

Query Match Best Local Similarity

99.0%;

Score 308.8; DB 25; Pred. No. 4.5e-53;

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27 - MIL - 2000;
28 - FEB - 2001;
29 - MIL - 2001;
20 - MIL - 2001;
20 - MIL - 2001;
21 - MOV - 1997;
22 - FEB - 1998;
23 - MAY - 1998;
24 - MAY - 1998;
25 - MAY - 1998;
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27 - MAY - 1998;
28 - MAY - 1998;
29 - MAY - 1998;
20 - JUN - 1998;
20 - JUN - 1998;
21 - J
                                            Ashkenazi AJ, Baker KP, Botstein D, Desnoyers L, Eaton
Ferrara N, Fong S, Gerber H, Gerritsen ME, Goddard A,
Grimaldi JC, Gurney AL, Kljavin IJ, Napier MA, Pan J,
Roy MA, Stewart TA, Tumas D, Watanabe CK, Williams PM,
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2000WO-US15264
2000WO-US15264
2000WO-US22031
2000WO-US233322
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2000WO-US233322
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2000WO-US217800
2001WO-US217800
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Godowski PJ;
RESULT 14
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AC ABX64
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Best Local S
Matches 310
                       cDNA encoding human PRO1245 polypeptide.
                                                                    26-FEB-2003
                                                                                                              ABX64209;
                                                                                                                                                         ABX64209 standard;
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                                                                  (first
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comprising a sequence without signal peptide and the nucleic acid comprising a sequence without signal peptide and the nucleic acid composition of the polypeptides can be used to raise antibodies that expecifically bind to the PRO polypeptide, for linking a bloactive come biological activity of a cell. The PRO polypeptides or modulating at least come biological activity of a cell. The PRO polypeptides or polynucleotides are also useful as pharmaceuticals, diagnostics, come biosensors or bioreactors, for detecting or treating e.g. tumours in commands, e.g. humans, dogs, cats, cattle, horses, sheep, pigs, goats or crabbits as targets for therapeutic intervention in certain cancers (e.g. colon, lung or breast cancers) and diagnostic determination of the presence of these cancers. The PRO polypeptides are also useful as completed as hybridisation probes or for screening libraries of human colon, genomic DNA or mRNA. The PRO genes may also be used in gene colon, persented in ABX79200-ABX90575 are the genes encoding, the primers can prifying and the probes detecting the PRO polynucleotides of the colon probes of the probes detecting the PRO polynucleotides of the colon probes of the probes detecting the PRO polynucleotides of the colon probes of the probes detecting the PRO polynucleotides of the colon probes of the probes detecting the PRO polynucleotides of the colon probes of the probes detecting the PRO polynucleotides of the colon probes of the probes detecting the PRO polynucleotides of the colon probes of the probes detecting the PRO polynucleotides of the colon probes of the probes detecting the PRO polynucleotides of the colon probes of the probes detecting the PRO polynucleotides of the probes detecting the probes detecting 
invention.

Note: The sequence data for this patent is also available in Note: The sequence data for this patent is also available in format from USPTO at seqdata.uspto.gov/sequence.html.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         The invention discloses isolated PRO secreted/transmembrane polypeptides comprising a sequence without signal peptide and the nucleic acid encoding them. The polypeptides can be used to raise antibodies that
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  New secreted and transmembrane PRO polypeptides (e.g. PRO183, PRO184, PRO361 or PRO846) useful as targets for therapeutic intervention in cancers (e.g. lung or breast cancers), or for diagnosing these cancers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 WPI; 2003-155950/15.
P-PSDB; ABU59026.
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                                                                                                                                                                             electronic
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Similarity ACAGTGTTTGGC 312 GAGCTGGGTCCCCAGGCCGTGGAGGGCCCTGAAGGCCCTGATGGGGCCCTGCTGGGGGCCCTGCTGGGGGCCCTGCTGAGGGCCCTGAGGCCCTGAGGCCCTGCTGGGGGCCCTGCTGGAGGCCCTGGAGGCCCTGGAGGCCCTGGAGGCCCTGGAGAGCCCTGGAGGCCCTGGAGGCCCTGGAGGCCCTGGAGGCCCTGGAGGCCCTGGAGGCCCTGGAGAGGCCCTGGAGGCCCTGGAGGCCCTGGAGGCCCTGGAGGCCCTGGAGGCCCTGGAGGCCCTGGAGGCCCTGGAGGCCCTGGAGGCCCTGGAGGCCCTGGAGGCCCTGGAGGCCCTGGAGGCCCTGGAGAGGCCCTGGAGGCCCTGGAGGCCCTGGAGGCCCTGGAGGCCCTGGAGGCCCTGGAGGCCCTGGAGGCCCTGGAGGCCCTGGAGGCCCTGGAGGCCCTGGAGGCCCTGGAGGCCCTGGAGGCCCTGGAGGCCCTGGAGGCCCTGGAGGCCCTGGAGGCCCTGGAGGCCCCTGGAGGCCCTGGAGGCCCTGGAGCCCTGGAGGCCCTGGAGGCCCTGGAGGCCCTGGAGGCCCTGGAGGCCCTGGAGGCCCTGGAGGCCCTGGAGGCCCCTGGAGGCCCTGGAGGCCCTGGAGGCCCTGGAGGCCCTGGAGGCCCTGGAGGCCCTGGAGGCCCTGGAGGCCCTGGAGGCCCTGGAGGCCCTGGAGGCCCTGGAGGCCCTGGAGGCCCTGGAGGCCCTGGAGGCCCTGGAGGCCCTGGAGGCCCTGGAGGCCCTGGAGGCCCCTGGAGGAGGCCCCTGGAGGGCCCTGGAGGCCCTGGAGGCCCTGGAGGCCCTGGAGGCCCCTGGAGGCCCCTGG 99.0%; ilarity 99.4%; Conservative Score 308.8; DB 25; Pred. No. 4.5e-53; 0; Mismatches 2; Indels Length 570; 0; Gaps 378 300 318 240 258 180 198 120 138

CDNA;

570

entry)

Human; PRO pol genetic disord gene therapy;

gene; ss.

US2002103125-A1

2001US - 0989731.

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PRO polypeptide; secreted c disorder; antibacterial;
98WO-US20069
98WO-US21930
98WO-US21141
98WO-US21141
98WO-US21169
99WO-US20106
99WO-US20109
99WO-US20109
99WO-US20109
99WO-US2009
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immunosuppressive; transgenic;
         REPRESENTED TO SOLUTION OF THE PROPERTY OF THE
                                    The present invention relates to the isolation of novel human PRO CC polypeptides, and the polynucleotide sequences encoding them. The CC prolypeptides are secreted and transmembrane proteins. The PRO CC linking bioactive molecules to cells expressing PRO polypeptides, for CC linking bioactive molecules to cells expressing PRO polypeptides, for CC polypeptides, and for for identifying agonists or antagonists. CC polypeptides, and for for identifying agonists or antagonists. CC hybridiation probes, in chromosome and gene mapping, in the generation CC of antisense RNA and DNA, in the preparation of PRO polypeptides, for CC polypeptides and for mapping the gene which encodes the PRO CC polypeptide, and for the generation analysis of individuals with genetic CC polypeptide, and for the genetic analysis of individuals with genetic CC disorders, in gene therapy, for chromosome identification, as chromosome markers, and for generating probes for PCR, Northern CC disorders, southern analysis and Western analysis. The present Note: The sequence data for this patent was obtained in electronic CC format directly from the USPTO web site at
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Ashkenazi AJ, Baker K
Ferrara N, Pong S, G
Grimaldi JC, Gurney A
Roy MA, Stewart TA,
Zhang Z;
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P-PSDB; ABU13986.
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98US-088033P

98US-088033P

98US-08825P

98US-088212P

98US-088212P

98US-088212P

98US-088212P

98US-088214P

98US-08824P

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98US-08824P

98US-08824P

98US-08824P

98US-08826P

98US-08861P

98US-08861P

98US-08861P

98US-089512P

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98US-089512P

98US-089513P

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98US-08953P
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      190
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   170
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other;
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Godowski : Paoni NF; Wood WI;

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15-SEP-1998
17-SEP-1998
17-SEP-1998
07-OCT-1998
05-JAN-1999
08-MAR-1999
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15-SEP-1999
15-SEP-1999
16-DEC-1999
17-MAR-2000
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RESUL ABX17 ID ABX17 ID XXX XXX XXX XXX XXX XXX XXX XXX XXX	Qui Be Ma Oy
MEXIT15 (ATT) (ABX17173; (A+FEB-2003) (first entry) (A+FEB-2004) (first entry) (A+FEB-2006) (first entry) (A	Query Match 99.0%; Score 308.8; DB 25; Length 570; Best Local Similarity 99.4%; Pred. No. 4.5e-53; Matches 310; Conservative 0; Mismatches 2; Indels 0; Gaps 1
PR 28-APR-1998; 98US-084322P: PR 07-MAY 1998; 98US-084700P: PR 28-MAY 1998; 98US-0877106: PR 28-MAY 1998; 98US-0877106: PR 28-MAY 1998; 98US-087709P: PR 02-JUN-1998; 98US-087627P: PR 02-JUN-1998; 98US-0808025P: PR 04-JUN-1998; 98US-0808025P: PR 04-JUN-1998; 98US-0808025P: PR 04-JUN-1998; 98US-0808025P: PR 04-JUN-1998; 98US-0808030P: PR 05-JUN-1998; 98US-0808021P: PR 05-JUN-1998; 98US-0808021P: PR 10-JUN-1998; 98US-0808021P: PR 10-JUN-1998; 98US-0808021P: PR 10-JUN-1998; 98US-0808021P: PR 11-JUN-1998; 98US-089910P: PR 11-JUN-1998; 98US-089931P: PR 11-JUN-1998; 98US-0899931P: PR 11-JUN-1998; 98US-0899931P: PR 11-JUN-1998; 98US-0899931P: PR 11-JUN-1998; 98US-0899931P: PR 11-JU	PR 24-FEB-2000; 2000WO-US01 PR 15-MAR-2000; 2000WO-US01 PR 15-MAR-2000; 2000WO-US01 PR 15-MAR-2000; 2000WO-US01 PR 15-MAR-2000; 2000WO-US01 PR 25-MAY-2000; 2000WO-US1 PR 27-MAY-2000; 2000WO-US1 PR 27-MAY-2000; 2000WO-US1 PR 27-MAY-2000; 2000WO-US1 PR 28-JUL-2000; 2000WO-US1 PR 28-JUL-2000; 2000WO-US1 PR 28-JUL-2000; 2000WO-US2 PR 28-JUL-2000; 2000WO-US2 PR 28-JUL-2000; 2000WO-US2 PR 28-JUL-2000; 2000WO-US2 PR 28-JUL-2000; 2000WO-US3 PR 29-JUL-2001; 2001WO-US3 PR 29-JUL-2001; 2001WO-US3 PR 29-JUL-2001; 2001WO-US3 PR 11-NUV-1997; 97US-062 PR 11-NUV-1997; 97US-062 PR 12-NUV-1997; 97US-065 PR 25-FEB-1998; 98US-075

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               The invention relates to a secreted and transmembrane polypeptide, termed CC PRO polypeptide, and the polypeptides according it. The polypeptide is CC useful for detecting, PRO polypeptides and for linking a bloactive conclude to a cell expressing the above polypeptides, where the bloactive molecule to a cell expressing the above polypeptides, where the bloactive causes the death of the cell. The polypeptide is useful for identifying cagonists or antagonists of the PRO polypeptide is useful for identifying candists or antagonists of the PRO polypeptide, for preparing variants of PRO, as a molecular weight marker for protein electrophoresis purposes cand the PRO polypuctide is useful for recombinantly expressing those concludes the polypuctide is useful for an antisation probe, in the preparation of propertide is also useful as a hybridisation probe, in the preparation of PRO polypeptide, for generating transgenic animals or knockout animals which in turn are useful in the development and concentrating of therapeitically useful reagents, to construct hybridisation probes for mapping the gene which encodes PRO and for the genetic canalysis of individuals with genetic disorders, in gene therapy, for probes for mapping the gene which encodes PRO and for the genetating canalysis of individuals with genetic disorders, in gene therapy, for probes for pcr, Northern analysis, Southern analysis and Western analysis. Northern analysis, Southern analysis and western in vention.
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Best Local Similarity
Matches 310; Conserv
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Novel secreted and transmembrane polypeptide for modulating biological activity of cell expressing the polypeptide, identifying agonists or antagonists of polypeptide, and as molecular weight markers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Ashkenazi AJ, Baker KP, Botstein D, Desnoyers L, Eaton DL; Ferrara N, Fong S, Gerber H, Gerritsen ME, Goddard A, Goddwski pJ; Grimaldi JC, Gurney AL, Kljavin IJ, Napier MA, Pan J, Paoni NF; RCY MA, Stewart TA, Tumas D, Watanabe CK, Williams PM, Wood WI;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        WPI; 2003-066810/06.
P-PSDB; ABU10941.
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ilarity 99.4%;
Conservative
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            2003,
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/cgn2_6/ptodata/2/pna/US092_COMB.seq:*
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/cgn2_6/ptodata/2/pna/US093_COMB.seq:*
/cgn2_6/ptodata/2/pna/US095_COMB.seq:*
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51: //ggn2_6/ptodata/2/pna/US101A_COMB.seq; *
52: //ggn2_6/ptodata/2/pna/US101A_COMB.seq; *
53: //ggn2_6/ptodata/2/pna/US101A_COMB.seq; *
54: //ggn2_6/ptodata/2/pna/US101A_COMB.seq; *
55: //ggn2_6/ptodata/2/pna/US101A_COMB.seq; *
56: //ggn2_6/ptodata/2/pna/US101A_COMB.seq; *
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58: //ggn2_6/ptodata/2/pna/US101A_COMB.seq; *
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

432H	Result No.
509.2 509.2 488.6 486	Score
92.4 92.4 88.7 88.2	Query
547 547 66743 13386	Length
1 45 99 101	80
1 PCT-USO2-05403-19 45 US-10-081-817-19 99 US-60-449-155-995 101 US-60-466-412-87918	
Sequence 19, Appl Sequence 19, Appl Sequence 995, App Sequence 87918, A	Description

60 60 N

120

```
RESULT 1

PCT -US02-05403-19

Sequence 19, Application PC/TUS0205403

GENERAL INFORMATION:

APPLICANT: Dana-Farber Cancer Institute, Inc.

APITE REFERENCE: 00530-094W01

CURRENT APPLICATION NUMBER: PCT/US02/05403

CURRENT APPLICATION NUMBER: PCT/US02/05403

CURRENT APPLICATION NUMBER: 60/270,973

PRIOR APPLICATION NUMBER: 60/270,973

PRIOR FILING DATE: 2001-02-23

PRIOR FILING DATE: 2001-02-23

PRIOR FILING DATE: 2001-01-25

NUMBER 0F SEQ ID NOS: 32

SOFTWARE: FastSEQ for Windows Version 4.0

SEQ ID NO 19

LENGTH: 547

TYPE: DNA

DENOTE: DNA

DE
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   Query Match
Best Local Similarity
                                                                                        NAME/KEY: misc_feature
LOCATION: 186
OTHER INFORMATION: n =
-US02-05403-19
                                                                                                                                                                                                        ORGANISM: Homo sapiens FEATURE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                338.4
338.4
1169.4
1169.8
1160.8
1143.6
1143.6
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5 US-10-059-579-120
5 US-10-059-579-120
5 US-10-059-579-120
5 US-10-059-579-120
1 US-09-710-175-431
2 US-08-790-774-9245
8 US-09-912-293-221180
7 US-09-634-3068-196114
4 US-10-027-632-196114
4 US-10-027-632-196114
5 US-09-770-175-4736
9 CT-US01-09339-8
9 CT-US01-09339-8
9 CT-US01-09339-8
10 US-09-549-342A-8
10 US-09-549-342A-8
11 US-09-549-342A-8
12 US-09-016-387-7
13 US-09-016-387-7
14 US-09-540-208-37787
18 US-09-016-387-3787
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US-09-720-533-199
US-10-242-799-18
US-10-426-002-18
US-09-016-387-6
US-09-927-796-27
US-10-211-858-27
US-10-211-858-27
US-09-949-238-407
US-09-941-992-407
      Score 509.2; DB Pred. No. 1e-76;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ALIGNMENTS
                             1;
                          Length
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Sequence 8431, Apsequence 221180, Apsequence 2211814, Sequence 8, Appli Sequence 1, Appli Sequence 1, Appli Sequence 6, Appli Sequence 1070, Apsequence 6, Appli Sequence 6, Appli Sequence 6, Appli Sequence 130, Appli Sequence 27, Appli Sequence 407, Appli Sequence 
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Sequence
Sequence
Sequence
Sequence
Sequence
Sequence
Sequence
                                                                                                                                                                                                                                                   Sequence 19, Application US/10081817
Sequence 19, Application US/10081817
Sequence 19, Application US/10081817
APPLICANT: POlyak, Kornelia
APPLICANT: Porter, Dale
APPLICANT: Sgroi, Dennis
APPLICANT: Krop, Ian
TITLE OF INVENTION: HIN-1, A TUMOR SUPPRESOR GENE
FILE REFERENCE: 00530-094001
CURRENT APPLICATION NUMBER: US/10/081,817
CURRENT FILING DATE: 2002-05-31
PRIOR APPLICATION NUMBER: 60/270,973
PRIOR APPLICATION NUMBER: 60/270,973
PRIOR FILING DATE: 2001-02-23
PRIOR FILING DATE: 2001-02-23
INUMBER OF SEQ ID NOS: 32
SOFTWARE: FastSEQ for Windows Version 4.0
SOFTWARE: FastSEQ for Windows Version 4.0
TYPE: DNA
DECANTOR.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       RESULT 2
US-10-081-817-19
                                                                                        ; OTHER INFORMATION: n = US-10-081-817-19
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Query Match
Best Local Similarity
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                                                                                                                                          ORGANISM: Homo sapiens FEATURE: NAME/KEY: misc_feature LOCATION: 186
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   361 GGCACGGCTTCCCAGGGCCCGCCGCCGCAGCAGGAAGTTGGCCAGGGCACGGCCGTG
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   92.4%;
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   Score 509.2; DB Pred. No. 1e-76;
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                             45;
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                          Length
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480 416 420 356 360

476

536

300

236 240

В

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; LENGTH: 66743
; TYPE: DNA
; ORGANISM: Human
US-60-449-155-995
                                                                                                                                                                                                                                                                                                     RESULT 3
US-60-449-155-995
                                                                                                                                                                          Sequence 995, Application US/60449155

Sequence 995, Application US/60449155

GENERAL INFORMATION:

APPLICANT: Keith, Tim

APPLICANTION: NUCLEOTIDE AND AMINO ACID SEQUENCES

TITLE OF INVENTION: RELATING TO RESPIRATORY DISEASES AND OBESITY

FILE REFERENCE: HUMO2-11P

CURRENT APPLICATION NUMBER: US/60/449,155

CURRENT FILING DATE: 2003-02-20

NUMBER OF SEQ ID NOS: 1000

SOFTWARE: FastSEQ for Windows Version 4.0

SEQ ID NO 995

SEQ ID NO 995
                                                                                                Query Match
Best Local S
Matches 529
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Matches
                                                     62043
            62103
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                                                                                             tch 88.7%;
al Similarity 95.8%;
529; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         61
                               61
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 1 CGGCCGGGAGGCGGCCGGGAGTGAGGCCTGATCGTCCCTGGCGCCTCCACCTCCCCAGG
                                                  CGGCCGGGAGGCGGCCGGGAGTGAGGCCTGATCGTCCCTGGCGCCTCCACCTCCCAGG
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                                                                                                                                                                                                                                                                                                                                                                                       CGCAGAAGGCGCCCACGAGGACCCCCAGTGCCCGACGTTGCCACGGTCTGGGATCAGAGG
                                                                                                                                                                                                                                                                                                                                              GCCCCGCGCC 551
GCCCCCGCGCC 547
                                                                                                                                                                                                                                                                                                                                                                                                                              AGCGGAGCGGGCAGGGCTTTCTCAGGAGCGCGGGCGAGGCCGGGCGCTGGAGGGGCGAGGAGGA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                         GGGCACGGGCTTCCCAGGGCCCGCCGGCCGCAGCAGGAACTTGGCCAGGCCACGGCCTGGCACGGCCTGGCACAGGCCACGGCCAGGCACGACACTTCCCAGGCCCGCCGCCGCCGCCGCAGCAGGAACTTGGCCAGGCAAGGACACGCCTG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 CTCTCTCAGAGGGCCCCAGCGCCTGCCAAGAGGAAGTCCTCGAGGGCCCGGGCAGGGAAGG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           AGACCGCAAAGCGAAGGTGCGGGCCGGGGTGGGCCTCGCGGAGACAAAGGCCGGGCCTGC
          CGCAGAAGGCGCCCACGAGGACCCCCAGTGCCCGACGTTGCCACGGTCTGGGATCAGAGG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Conservative
                                                                                             Score 488.6; DB 99;
Pred. No. 1.8e-73;
0; Mismatches 5;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             8
                                                                                              Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Indels
                                                                                                                 Length 66743;
                                                                                              18; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             4;
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                                                  62102
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                                                                                                                                                                                        Sequence 87918, Application US/60466412

GENERAL INFORMATION:
APPLICANT: CARGILL, Michele
APPLICANT: LAKOUBOVA, Olga
TITLE OF INVENTION: MYCHAICA INFARCTION, METHODS OF DETECTION AND USES THEREOF
FILE REFERENCE: CLOO1466
CURRENT FILING DATE: 2003-04-30
NUMBER OF SEQ ID NOS: 429241
SOUTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 87918
LENGTH: 13386
TYPE: DNA
ORGANISM: Homo sapiens
FEATURE:
NAME/KEY: misc_feature
LCCATION: (1)...(13386)
OTHER INFORMATION: n = A,T,C or G
US-60-466-412-87918
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Best Local S
Matches 528
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                  GGGGCACGGGCTTCCCAGGGCCCGCCGGCCGCAGCAGGAAGTTGGCCAGGGCACGGCCGT
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                                                                                                                                                 88.2%;
ilarity 95.7%;
Conservative
                                                                                                                                                Score 486; DB 101;
Pred. No. 5.9e-73;
O; Mismatches 5;
                                                                                                                                                  Indels
                                                                                                                                                                      Length 13386;
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                                                                                                                                                  Gaps
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US-60-213-178-297/c

Sequence 297, Application US/60213178

Sequence 297, Application US/60213178

SEQUENCE INFORMATION:

TITLE OF INVENTION: ISOLATED HUMAN KINASE PROTEINS, NUCLEIC

TITLE OF INVENTION: ACID MOLECULES ENCODING HUMAN KINASE PROTEINS, AND USES

TITLE OF INVENTION: THEREOF

FILE REFERENCE: CL00689

CURRENT APPLICATION NUMBER: US/60/213,178

CURRENT FILING DATE: 2000-06-22

NUMBER OF SEQ ID NOS: 1425

SOFTWARE: FastSEQ for Windows Version 4.0

SEQ ID NO 297

LENGTH: 32768
                                                                                                                                                                                                                                                                                                                                                    LENGTH: 32768

TYPE: DNA
ORGANISM: Human
FEATURE:
NAME/KEY: misc_feature
LOCATION: (1)...(32768)
OTHER INFORMATION: n 4 A,
US-60-213-178-297
                                                                                                                                                                                                                                                                                                          Query Match
Best Local Similarity
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                                            ACCGGGTATAAGAAGCTCGTGGCCTTGCCCGGGCAGCCGCAGGTTCCCCGCGCGCCCCG
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                                                                                                                                                                                                                                                                                                        95.7%;
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                                                                                                                                                                                                                                                                                          Score 486; DB 75; Length 32768;
Pred. No. 5.3e-73;
0; Mismatches 5; Indels 19;
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SEGNERAL INFORMATION:
APPLICANT: THE JOHNS HOPKINS UNIVERSITY SCHOOL OF NAPPLICANT: SUKUMAR, Saraswati
APPLICANT: SUKUMAR, Saraswati
APPLICANT: DOLDEY, William C.
APPLICANT: DOLDEY, William C.
APPLICANT: DAVIDSON, Mancy
Jo.
APPLICANT: DAVIDSON, Mancy
APPLICANT: DAVIDSON, MAS JO.
FILE REFERENCE: JHU1630-1
CURRENT APPLICATION NUMBER: US/10/059,579
CURRENT FILING DATE: 2003-02-03
PRIOR APPLICATION NUMBER: US 99/771,357
PRIOR APPLICATION NUMBER: US 09/771,357
PRIOR FILING DATE: 2001-01-26
SOFTWARE: Patentin version 3.1
SEQ ID NO 120
LENGTH: 1794
                                                                                                                                                                                                                                                                                                                                                   ; TYPE: DNA
; ORANIA: Homo sapiens
; EEATURE:
; NAME/KEY: misc_feature
; LOCATION: (359)..(359)
; OTHER INFORMATION: n is any nucleotide
US-10-059-579-120
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Best Local
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                                                                                                                                                                                                                                                          Similarity
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GGCAGGGCTTTCTCAGGAGCGCGGGCGAGGCCGGCGCTGGAGGGCGAGGACCGGGTATA
                                            AGGGCCCCAGCGCCTGCCAAGAGGAAGTCCTCGAGGCCCGGGCAGGGAAGGGGGCACGGG 369
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ilarity 97.8%;
Conservative
                                                                                                                                                                                                                                                                                        0;
                                                                                                                                                                                                                                                                                                     Score 338.4; DB 45; Pred. No. 6.9e-48;
                                                                                                                                                                                                                                                                                          Mismatches
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US-10-059-579A-120

Sequence 120, Application US/10059579A

Sequence 120, Application US/10059579A

GENERAL INFORMATION:
GENERAL INFORMATION:
APPLICANT: THE JOHNS HOPKINS UNIVERSITY SCHOOL OF MEDICINE
APPLICANT: SUKUMAR, Saraswati
APPLICANT: EVROW, Ella
APPLICANT: DOOLEY, William C.
APPLICANT: DAVIDSON, Mancy
APPLICANT: DAVIDSON, MANCY
TITLE OF INVENTION: ABERRANTLY METHYLATED GENES AS MARKERS OF BREAST MALIGNANCY
TITLE OF INVENTION: ABERRANTLY
TITLE OF INVENTION: ABERRANTLY
TITLE OF INVENTION: ABERRANTLY
TITLE OF INVENTION: ABERRANTLY
TITLE OF INVENTION: UNMBER: US/10/059,579A

CURRENT FILING DATE: 2002-01-28
PRIOR APPLICATION NUMBER: US 09/771,357
PRIOR APPLICATION NUMBER: US 09/771,357
PRIOR FILING DATE: 2001-01-26
NUMBER OF SEQ ID NOS: 136
SOFTWARE: Patentin version 3.1
SEQ ID NO 120
LENGTH: 1794
TYPE: DNA
ORGANISM: Homo saplens
FEATURE:
NAME/KEY: misc_feature
US-10-059-579A-120
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US-10-059-579A-120
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Best Local (
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1110 AGAAGCCTCGTGGCCTTGCCCGGGCAGCCCCAGGTTCCCCGCGCGCCCCGAGCCCCCGCG 1169
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Similarity
                                                                                                                                                                                                                 CTTCCCACGGCCCGCCGCCGCAGCAGGAAGTTGGCCAGGGCACGGCCGTGAGCGGAGCG 429
                                                                                                                                                                                                                                                                               AGAAGCCTCGTGGCCTTGCCCGGGCAGCCGCAGGTTCCCCGGGGCGCCCGAGCCCCCGCG 549
                                                                                     CC 551
                         CC 1171
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                61.4%;
ilarity 97.8%;
Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Score 338.4; DB 45; Length 1794; pred. No. 6.9e-48; 0; Mismatches 6; Indels 2;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Gaps
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APPLICANT: Shyjan, Andrew W.
APPLICANT: Stbdal, Hilde
APPLICANT: Shyjan, HOVEL NUCLEIC ACID MOLECULES AND
TITLE OF INVENTION: THEREFOR
TITLE OF INVENTION: THEREFOR
TITLE OF INVENTION: UNUMER: US/09/710,281
CURRENT FILING DATE: 2000-11-10
CURRENT FILING DATE: 2000-11-09
PRIOR APPLICATION NUMBER: 60/164,254
PRIOR APPLICATION NUMBER: 60/164,254
PRIOR FILING DATE: 1999-11-09
PRIOR FILING DATE: 1999-11-09
PRIOR FILING DATE: 1999-11-09
PRIOR FILING DATE: 5803
SOFTWARE: FESTERG for Windows Version 4.0
SEQ ID NO 4055
LENGTH: 627
                                                                                                                                                                                                                                                                  Sequence 8431, Application US/09770175

GENERAL INFORMATION:

APPLICANT: Gearing, David P.

APPLICANT: Holtzman, Douglas A.

APPLICANT: Holtzman, Douglas A.

TITLE OF INVENTION: THEREFOR

TITLE OF INVENTION: THEREFOR

TITLE OF INVENTION UNMERS: US/09/770,175

CURRENT APPLICATION NUMBER: US/09/770,175

CURRENT APPLICATION NUMBER: US 60/178,874

PRIOR APPLICATION NUMBER: US 60/178,874

PRIOR FILING DATE: 2000-01-28

NUMBER OF SEQ ID NOS: 8967

SOFTWARE: FastEEQ for Windows Version 4.0

SOFTWARE: FastEEQ for Windows Version 4.0

TYPE: DNA

ORGANITAN: Homo saniang
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US-09-770-175-8431
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Best Local Similarity 96.6
Matches 173; Conservative
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Best Local S
Matches 173
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      493
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         433
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              131
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          71
                                                                                                              173;
                   493
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          AGCCTCGTGGCCTTGCCCGGGCAGCCGCAGGTTCCCCGCGCGCCCGAGCCCCGCGCC 551
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        AGGGCTTTCTCAGGAGCGCGGGCGAGGCCGGCGCTGGAGGGGCGAGGACCGGGTATAAGA 492
                                                                                                                                                                                                Similarity
                                                AGGGCTTTCTCAGGAGCGCGGGCGAGGCCGGCGCTGGAGGGGCGAGGACCGGGTATAAGA 492
AGCCTCGTGGCCTTGCCCGGGCAGCCGCAGGTTCCCCGCGCGCCCCGAGCCCCCGCGCCCC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Application US/09710281
                                                                                                                                                                                    Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            30.7%;
                                                                                                                                                                                                    30.7%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Score 169.4; DB 31; pred. No. 3e-19; 0; Mismatches 6;
                                                                                                                                                                                    Score 169.4; DB 33; pred. No. 3e-19; 0; Mismatches 6;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Length 627;
                                                                                                                                                                                                                             Length 714;
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RESULT 8

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RESULT 11
US-09-912-293-221180
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US-08-790-774-9245
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TELEFAX: (301) 309-8512
INFORMATION FOR SED ID NO: 92.
SEQUENCE CHARACTERISTICS:
LENGTH: 210 base, pairs
TYPE: nucleic acid
STRANDEDNESS: double
TOPOLOGY: linear
                                                                                                                                              Sequence 221180, App
GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Sequence 9245, Appli
GENERAL INFORMATION
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Query Match
              CURRENT APPLICATION NUMBER: US/09/912,293
CURRENT FILING DATE: 2001-07-26
PRIOR APPLICATION NUMBER: 08/103,744
PRIOR FILING DATE: 1993-08-09
                                                                                     APPLICANT: Rosen, et. al.
TITLE OF INVENTION: Human Genes, Sequences,
FILE REFERENCE: PO-100
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        APPLICATION NUMBER: U5/08/790,7:
FILING DATE: JAN-30-1997
CLASSIFICATION: |536
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 60/010,822
APPLICATION NUMBER: 9-1996
ATTORNEY/AGENT INFORMATION:
NAME: Michale M. Wales
REGISTRATION NUMBER: P-43,975
REFERENCE/DOCKET NUMBER: P-020
TELECOMMUNICATION INFORMATION:
TELECHNUMICATION INFORMATION:
TELECHNUMICATION INFORMATION:
TELECHNUMICATION INFORMATION:
TELECHNUMICATION SECONDATION:
PRIOR
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SOFTWARE: ASCII Text
CURRENT APPLICATION DATA:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TITLE OF INVENTION: Hun
NUMBER OF SEQUENCES: 97
CORRESPONDENCE ADDRESS:
ADDRESSEE: Human Genc
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   COUNTRY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         CITY: Rockville
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            STREET:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Loca1
APPLICATION NUMBER: 09/249,651
                                                                                                                                                                                                                                                                                                494
                                                                                                                                                                                                                                                                                                                                                       434 GGGCTTTCTCAGGAGCGCGGCGAGGCCGGCGCTGGAGGGGCGAGGACCGGGTATAAGAA 493
                                                                                                                                                                                                                                                             129
                                                                                                                                                                                                                                                                                                                                                                                                                                                 374 CCAGGGCCGGCGGCGCAGCAGGAAGTTGGCCAGGGCACGGCCGTGAGCGGAGCGGGCA 433
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    tch | 29.2%;
al Similarity | 91.0%;
162; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   131
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                                                                                                                                                                                                                                                         GGGGNTTCTCAGNNNCGCGGGCGAGGCCGGCGCTNGAGGGGCGAGGACCGGGTATAAGAA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Maryland
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        E: Human Genome Sciences,
9410 Key West Avenue
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     USA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            E: Diskette, 3.50 inch, 1.4Mb
HP Vectra 486/33
                                                                                                                                                                 Application US/09912293
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            UMBER: US/08/790,774
JAN-30-1997
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      A. Rosen
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Human Genes, Sequences, and Expression Products 9715
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         MSDOS version 6.2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          60/010,822
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             9245:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Score 160.8; DB 12; Pred. No. 9.7e-18; D; Mismatches 16;
                                                                                                          and Expression Products
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          DB 12;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Length 210;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Gaps
            ; FEATURE:
NAME/KEY: misc_feature
LOCATION: (200)...(200)
OTHER INFORMATION: n is
US-09-912-293-221180
                                                                                                                                                                                                                                                       NAME/KEY: misc_feature
LOCATION: (142)..(142)
OTHER INFORMATION: n is
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     FEATURE:
                                                                                                                           NAME/KEY: misc_feature
LOCATION: (185)..(185)
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                                                                                                                                                                 FEATURE
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       NAME/KEY: misc_feature LOCATION: (81)..(83)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        PEATURE
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PRIOR APPLICATION NUMBER: 08/21,623
PRIOR FILING DATE: 1994-02-15
PRIOR FILING DATE: 1994-03-31
PRIOR FILING DATE: 1994-03-31
PRIOR APPLICATION NUMBER: 08/220,691
PRIOR APPLICATION NUMBER: 08/220,691
PRIOR APPLICATION NUMBER: 08/741,830
PRIOR APPLICATION NUMBER: 09/741,830
PRIOR APPLICATION NUMBER: 09/813,155
PRIOR FILING DATE: 2001-03-21
PRIOR FILING DATE: 2001-03-21
PRIOR FILING DATE: 2010-03-21
Remaining Prior Application data removed - See File Wrapper or PALM.
NUMBER OF SEQ ID NOS: 244538
SEQ ID NO 221180
LENGTH: 210
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  PRIOR FILING DATE: 1999-02-12
PRIOR APPLICATION NUMBER: 08/104,507
PRIOR FILING DATE: 1993-08-09
PRIOR APPLICATION NUMBER: 08/196,363
PRIOR FILING DATE: 1994-02-15
PRIOR APPLICATION NUMBER: 09/859,490
PRIOR FILING DATE: 2001-05-18
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ORGANISM: Homo sapiens

NAME/KEY: misc_feature LOCATION: (12)...(12) OTHER INFORMATION: n is equal to a,t,g, ဝူ o

NAME/KEY: misc_feature LOCATION: (61)..(62) LOCATION: (15)..(15)
OTHER INFORMATION: n is NAME/KEY: misc_feature LOCATION: (15)..(15) equal equal ť a,t,g, or O a

OTHER INFORMATION: n is NAME/KEY: misc_feature LOCATION: (66)..(66) equal ç ç a,t,g, or a,t,g, or

OTHER INFORMATION: n is NAME/KEY: misc_feature LOCATION: (73)..(73) equal б a

NAME/KEY: misc_feature LOCATION: (103)..(103) COTHER INFORMATION: n is equal б ç a,t,g, or a, t, g, O

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OTHER INFORMATION: n is NAME/KEY: misc_feature LOCATION: (138)..(138) equal ç a,t,g, ç ი

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NAME/KEY: misc_feature LOCATION: (155)..(155) OTHER_INFORMATION: n is equal ţ ç a,t, a,t,g, or c ģ O

LOCATION: (185)..(185)
OTHER INFORMATION: n is equal to a,t,g, or ç a,t,g, a

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REMERAL INFORMATION:
APPLICANT: Wang, David G.
TITLE OF INVENTION: Identification and Mapping of Single Nucleotide
FILE REFERENCE: 10827.129
CURRENT APPLICATION NUMBER: US/09/634,306B
CURRENT FILING DATE: 2002-02-21
PRIOR APPLICATION NUMBER: US 60/218,006
PRIOR APPLICATION NUMBER: US 60/218,006
PRIOR APPLICATION NUMBER: US 60/198,676
PRIOR APPLICATION NUMBER: US 60/193,483
PRIOR APPLICATION NUMBER: US 60/193,483
PRIOR APPLICATION NUMBER: US 60/193,483
PRIOR APPLICATION NUMBER: US 60/185,218
PRIOR APPLICATION NUMBER: US 60/185,218
PRIOR APPLICATION NUMBER: US 60/185,218
PRIOR APPLICATION NUMBER: US 60/185,358
PRIOR APPLICATION NUMBER: US 60/185,358
PRIOR APPLICATION NUMBER: US 60/167,363
PRIOR APPLICATION NUMBER: US 60/166,358
PRIOR APPLICATION NUMBER: US 60/166,358
PRIOR APPLICATION NUMBER: US 60/166,002
PRIOR APPLICATION NUMBER: US 60/167,363
PRIOR FILING DATE: 1999-01-28
PRIOR APPLICATION NUMBER: US 60/167,363
PRIOR FILING DATE: 1999-01-29
PRIOR APPLICATION NUMBER: US 60/167,363
PRIOR FILING DATE: 1999-01-29
PRIOR APPLICATION NUMBER: US 60/167,363
PRIOR FILING DATE: 1999-01-29
PRIOR APPLICATION NUMBER: US 60/167,363
PRIOR FILING DATE: 1999-01-29
PRIOR APPLICATION NUMBER: US 60/167,363

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US-09-634-306B-196114/c
US-09-634-306B-196114, Application US/09634306B
; GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ; ORGANISM: Human
US-09-634-306B-196114
RESULT 13
US-10-027-632-196114/c
; Sequence 196114, Application US/10027632
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Best Local (
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Query Match
Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      374 CCAGGGCCCGCCGGCCGCAGCAGGAAGTTGGCCAGGGCACGGCCGTGAGCGGAGCGGGCA 433
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       162;
                                                                                                                                                                                                                                                                                                                                                    180 TCCCTCACCNG 190
                                                                                                                                                                                                                                           181;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                CGGCCGGGAGGCGGCCGGGAGTGAGGCCTGATCGTCCCTGGCGCCTCCACCTCCCCAGG 60
                                                                                                                                        TCCCTCACCGG 3
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91.0%;
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Pred. No. 9.7e-18;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Score 143.6; DB 27; Length 533; Pred. No. 7.1e-15; O; Mismatches 5; Indels 5;
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RESULT 14

US-09-770-175-4736

Sequence 4736, Application US/09770175

Sequence 4736, Application US/09770175

Sequence 4736, Application US/09770175

GENERAL INFORMATION:
APPLICANT: HOILZMAN, Douglas A.
TITLE OF INVENTION: NOVEL NUCLEIC ACID MOLECULES AND USES
TITLE OF INVENTION: THEREOR
FILE REFERENCE: 1600.2058-001
CURRENT APPLICATION UNMBER: US/09/770,175
CURRENT APPLICATION NUMBER: US/60/178,874
PRIOR APPLICATION NUMBER: US 60/178,874
PRIOR FILING DATE: 2000-01-28
NUMBER OF SEQ ID NOS: 8967
SOFTWARE: FASTSEQ for Windows Version 4.0
SEQ ID NO 4736
LENGTH: 624
TYPE: DNA
ORGANISM: Homo sapiens
FEATURE:
NAME/KEY: misc_feature
LOCATION: (1)...(624)
OTHER INFORMATION: n = A,T,C or G
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              GENERAL INFORMATION:

APPLICANT: Wang, David G.

FILE OF INVENTION: Identification and Mapping of Single Nucleotide

FILE REFERENCE: 108827.129

CURRENT FILING DATE: 2002-04-30

PRIOR APPLICATION NUMBER: US 60/218,006

PRIOR FILING DATE: 2000-07-12

PRIOR FILING DATE: 2000-07-12

PRIOR FILING DATE: 2000-03-29

PRIOR APPLICATION NUMBER: US 60/193,483

PRIOR FILING DATE: 2000-02-24

PRIOR APPLICATION NUMBER: US 60/193,483

PRIOR FILING DATE: 2000-02-24

PRIOR APPLICATION NUMBER: US 60/193,483

PRIOR APPLICATION NUMBER: US 60/193,483

PRIOR APPLICATION NUMBER: US 60/193,483

PRIOR APPLICATION NUMBER: US 60/193,363

PRIOR APPLICATION NUMBER: US 60/195,318

PRIOR APPLICATION NUMBER: US 60/185,218

PRIOR APPLICATION NUMBER: US 60/185,363

PRIOR APPLICATION NUMBER: US 60/167,363

PRIOR APPLICATION NUMBER: US 60/167,363

PRIOR APPLICATION NUMBER: US 60/156,358

PRIOR FILING DATE: 1999-01-23

PRIOR FILING DATE: 1999-09-28

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Best Local
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           121 CA-GGGACCAGGGAGCCAGGAACTGCGCCGCCCCCGCCCCTGCCCTGGCGCGAGGGAACC 179
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              69 CACGGGACCAGGAGCCAGGAACTGCGCCC---CGCCCTGCCTGGCGCGA-GGAAGC
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Pred. No. 7.1e
0; Mismatches
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CURRENT APPLICATION NUMBER: CCT/USO1/09339

CURRENT FILING DATE: 2001-03-22

PRIOR APPLICATION NUMBER: US 09/467,602

PRIOR APPLICATION NUMBER: US 09/215,818

PRIOR APPLICATION NUMBER: US 09/215,818

PRIOR APPLICATION NUMBER: US 08/912,276

PRIOR PILING DATE: 1998-12-18

PRIOR APPLICATION NUMBER: US 08/697,105

PRIOR FILING DATE: 1997-08-17

PRIOR APPLICATION NUMBER: US 08/912,149

PRIOR FILING DATE: 1997-08-19

PRIOR APPLICATION NUMBER: US 08/697,106

PRIOR APPLICATION NUMBER: US 08/697,106

PRIOR PRIOR APPLICATION NUMBER: US 08/697,106

PRIOR PRIOR PILING DATE: 1995-08-19

SEO ID NO SEO ID NOS: 12

SOFTWARE: FastSEQ for Windows Version 4.0

SEQ ID NO SEQ ID NOS 12

TYPE: DNA

ORGANISM: Homo sapiens

FEATURE:

NAME/KEY: misc_feature
LOCATION: (17)...(17) |

OTHER INFORMATION: n = a or g or c or t/u, unknown or other at

OCHER INFORMATION: position 17

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PCT-US01-09339-8
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Matches 120
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Best Local
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         APPLICANT: Colpitts, Tracey L.
APPLICANT: Russell, John C.
TITLE OF INVENTION: REAGENTS AND METHODS USEFUL FOR
TITLE OF INVENTION: DETECTING DISBASES OF THE REPRODUCTIVE TISSUES
FILE REFERENCE: 5972.U$.P6
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        APPLICANT: Abbott Laboratories APPLICANT: Colpitts, Tracey L APPLICANT: Russell, John C.
                                                                                                                          492 ANGCCTGGGCCTTGCCCGGG--CAGCCCCAGGTTCCCCGC 531
127 ANGCCTCGTGGCCTGCCCGGGTCANGCCGNANGTTCCCCGC 168
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al Similarity 99.2%;
120; Conservative
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                             551 C 551
                                                           al Similarity
150; Conserv
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Pred. No. 1.8e-11;
0; Mismatches 9; Indels 3;
                                                                                                                                                                                          Score 120; DB 1;
pred. No. 6.9e-11;
0; Mismatches 1
                                                                                                                                                                                          1; Indels
                                                                                                                                                                                                                        Length 562;
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Search completed: September 20, 2003, 03:12:36 Job time: 3508.06 secs

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September 20,

Copyright

Title: Perfect score:

Scoring table:

Minimum DB Maximum DB

seq seq

length: 0 length: 2000000000

Database

Result

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Length

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99.8 551 9.5 1433 9.5 14727 9.5 14782 9.5 16525 9.0 2368 9.0 1216 8.9 65518 8.9 121612 8.9 121612 8.9 2475 8.6 2475 8.6 22475 8.6 22491 8.2 72332 8.2 72332 8.2 72332 8.2 72332 8.3 160476 8.1 60476 8.1 62312 8.1 62312 8.1 4813647 7.9 185257

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Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries
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score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.
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1 cggccggggaggccggg......gcgccccgagccccgcgcc 551
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1: /cgn2_6/ptodata/1/pna/PCT_NEW_COMB.seq:*

2: /cgn2_6/ptodata/1/pna/US06_NEW_COMB.seq:*

3: /cgn2_6/ptodata/1/pna/US08_NEW_COMB.seq:*

4: /cgn2_6/ptodata/1/pna/US08_NEW_COMB.seq:*

5: /cgn2_6/ptodata/1/pna/US08_NEW_COMB.seq:*

6: /cgn2_6/ptodata/1/pna/US09_NEW_COMB.seq:*

6: /cgn2_6/ptodata/1/pna/US09_NEW_COMB.seq:*

7: /cgn2_6/ptodata/1/pna/US09_NEW_COMB.seq:*
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S US-10-081-817A-19
PCT-US03-21379-7
1US-60-487-610-1981
1US-60-487-610-1981
1US-60-485-114A-2674
1US-60-485-114-16671
1US-60-495-114-16671
1US-60-495-114-1685
1PCT-US03-1231-113
1US-60-495-114-2623
1US-60-495-114-2623
1US-60-495-114-2623
1US-60-495-114-2623
1US-60-495-114-2633
1US-60-495-114-2633
1US-60-497-113-58
1US-60-497-113-58
1US-60-497-518-15
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Compugen Ltd
      Sequence 19, Appl Sequence 3443, A Sequence 1991, Appl Sequence 1991, Appl Sequence 2674, Appl Sequence 2674, Appl Sequence 2677, Appl Sequence 16875, Appl Sequence 16875, Appl Sequence 16875, Appl Sequence 16805, Appl Sequence 16805, Appl Sequence 16805, Appl Sequence 16806, Appl Sequence 1437, Appl Sequence 1437, Appl Sequence 15232, Appl Sequence 15243, Appl Sequence 15243, Appl Sequence 15624, Appl Sequence 16591, Appl Sequence 16591, A Sequence 1591, Appl Sequence 1594, Appl Sequence 1591, Appl Sequence 1594, Appl S
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; Sequence 19, Application US/10081817A
; Sequence 19, Application US/10081817A
; Sequence 19, Application US/10081817A
; APPLICANT: POLYAK, Kornelia
APPLICANT: Syroi, Dala
APPLICANT: STOP, IBA
APPLICANT: KTOP, IBA
APPLICANT: KTOP, IBA
TITLE OF INVENTION: HIM-1, A TUMOR SUPPRESSOR GEN
TITLE REFERENCE: 10530-094001
; FILE REFERENCE: 10530-094001
; FILE REFERENCE: 10530-094001
; FILE REFERENCE: 10530-094001
; FILE REFERENCE: 1050-02-22
; COURSENT FILING DATE: 2002-02-23
; PRIOR APPLICATION NUMBER: US 60/270,973
PRIOR APPLICATION UMMBER: US 60/351,908
; PRIOR FILING DATE: 2002-01-25
; NUMBER OF SEQ ID NOS: 32
; SOFTWARE: FEASTSEQ for Windows Version 4.0
; SEQ ID NO 19
; SEQ ID NO 19
; SEQ ID NO 19
; LENGTH: 551
; NAME/KEY: misc_feature
; NAME/KEY: misc_feature
; COCATION: 1890-684019: C or G
US-10-081-817A-19
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US-10-081-817A-19
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Best Local Similarity
Matches 551; Conserv
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1 CGGCCGGGGAGGCGGGAGTGAAGGCCTGATCGTCCCTGGCGCCTCCACCTCCCAGG
1 CGGCCGGGGAGGCGGCGGGAGTGAAGGCCTGATCGTCCCTGGGCGCCTCCACCTCCCAGG
                                                                                                                                                                                                                 CGCAGAAGGCGCCCACGAGGACCCCCAGTGCCCGACGTTGCCACGGTCTGGGATCAGAGGCGCCAGAAGGCGCCCACGAGGTCTAGGATCAGAGGCGCCAGAAGGCGCCCACGAGGTGCCGACGTTGCCACGGTCTGGGATCAGAGGCGCAAGAAGGCGCCCACGAGGAGCCCCAGGTGCCCACGTTGCCACGGTCTGGGATCAGAGG
                                                               CCCTCACCNGAGGGAAGCTCCCCTCACCCGGCCCAGCCCTGCAGGGGGGGCGCGTGGGGTC
                           AGACCGCAAAGCGAAGGTGCGGGCCGGGGTGGGCCTCGCGGAGACAAAGGCCGGGCCTGC
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illarity 100.0%;
Conservative (
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US-10-425-114A-31613
US-10-425-114A-26232
US-10-425-114A-26232
US-00-487-610-19371
US-60-485-114-16936
US-60-485-114-16936
US-60-495-114-16936
US-60-495-114-15371
US-60-495-114-15371
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US-60-487-610-19525
US-60-487-610-19525
US-60-487-610-19525
US-60-487-610-19483
US-60-487-610-12483
US-60-495-114-16474
US-60-487-610-12483
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                                                                                                                                                                                                                                                                                                                                                       DB 6; ... 3.8e-100; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                     Length 551;
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Sequence 31022, A
Sequence 31613, A
Sequence 26232, A
Sequence 26232, A
Sequence 19371, A
Sequence 11932, A
Sequence 16948, A
Sequence 16448, A
Sequence 2710, App
Sequence 589, App
Sequence 16371, A
Sequence 16371, A
Sequence 19525, A
Sequence 19483, A
Sequence 11443, A
Sequence 12443, A
Sequence 12443, A
Sequence 12443, A
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CURRENT APPLICATION NUMBER: PCT/US03/21379
CURRENT FILING DATE: |2003-07-09
PRIOR APPLICATION NUMBER: US 60/394,845
PRIOR FILING DATE: 2002-07-10
PRIOR FILING DATE: 2002-07-10
PRIOR FILING DATE: 2002-09-16
PRIOR FILING DATE: 2002-09-16
PRIOR FILING DATE: 2002-09-16
VALUE OF SEQ ID NOS: |100
SOFTWARE: PATENTIN VETSION 3.2
SEQ ID NO 7
SEQ ID NO 7
LENGTH: 1133
TYPE: DNA
ORGANISM: HOMO Saplen's
PCT-US03-21379-7
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     RESULT 2
PCT-US03-21379-7/c
; Sequence 7, Application PC/TUS0321379
; GENERAL INFORMATION:
; APPLICANT: EXELIXIS, INC.
; TITLE OF INFERRENCE: EX03-047C-PC
; FILE REFERENCE: EX03-047C-PC
; FILE REFERENCE: EX03-047C-PC
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Best Local Similarity | 49.8%;
Matches 160; Conservative
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                                           CGCGCCCGAGCCCCCGCGCC 551
                                                                                            GGGGCGAGGACCGGGTATAAGAAGCCTCGTGGCCTTGCCCGGGCAGCCAGGTTCCCCG
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                                                                       CCCCCCGGGCGCTCCGGGTCCGCCGCGCAGGTCGGC--CAGGATGCTGGCGGCCAGCA
                                                                                                                                                                                                                               CTCTCTCAGAGGGCCCCAGCGCCTGCCAAGAGGAAGTCCTCGAGGCCCGGGCAGGGAAGG
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Pred. No. 0.064;
0; Mismatches 159;
                  92
                                                                                                                                                                                                                                                                                                                                                              Length 1133;
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RESULT 4
US-60-487-610-19981
; Sequence 19981, Application US/60487610
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US-10-425-114A-33423/c

Sequence 33423, Application US/10425114A

EGRERAL INFORMATION:

APPLICANT: Liu, Jingdong
APPLICANT: Liu, Jingdong
APPLICANT: Enou, Yihua
APPLICANT: Kovalic, David K.
APPLICANT: Screen, Steven E
APPLICANT: Tabaska, Jack E

APPLICANT: Tabaska, Jack E

APPLICANT: Cao, Yongwei
TITLE OF INVENTION: Nucleic Acid Molecules and Other Molecules Associated With
TITLE OF INVENTION: Plants and Uses Thereof for Plant Improvement
FILE REFERENCE: 38-21(53313)B
CURRENT APPLICATION NUMBER: US/10/425,114A
CURRENT APPLICATION NUMBER: US/10/425,114A
CURRENT FILING DATE: 2003-04-28
NUMBER OF SEQ ID NO3423
LENGTH: 1431
TYPE: DNA
ORGANISM: Zea mays
FEATURE: Load mays
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les 244; Conserv
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                        CGCGCC 551
                                                                         AGCGGGCAGGGCTTTCTCAGGAGGCGGGGCGAGGCCAGGCCCTGGAGGGGCGAGGACCGGG
                                                                                                                                                                      GGCTTCCCAGGGCCCGCCGCCC--AGCAGGAAGTTGGCCAGGGCACGGCCGTGAGCGG
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ilarity 44.7%;
Conservative
134
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Pred. No. 0.066;
0; Mismatches 300; Indels 2
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RESULT 5
US-60-487-610-1384
; Sequence 1384, Ap
; GENERAL INFORMATI
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; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: (1)...(147727)
; OTHER INFORMATION: n = A
US-60-487-610-19981
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ORGANISM: Homo sapiens
US-60-487-610-1384
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APPLICANT: CARGILL, Michele
APPLICANT: HUANG, Hongjin
TITLE OF INVENTION: GENETIC POLYMORPHISMS ASSOCIATED WITH
TITLE OF INVENTION: LIVER FIBROSIS IN HEPATITIS C VIRUS-INFECTED SUBJECTS,
TITLE OF INVENTION: METHODS OF DETECTION AND USES THEREOF
FILE REFERENCE: CL001469
CURRENT APPLICATION NUMBER: US/60/487,610
CURRENT FILING DATE: 2003-07-17
NUMBER OF SEO ID NOS: 97101
SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 19981
LENGTH: 147727
                    Sequence 1384, Application US/60487610

Sequence 1384, Application US/60487610

GENERAL INFORMATION:
APPLICANT: LIVENTION: GENETIC POLYMORPHISMS ASSOCIATED WITH
TITLE OF INVENTION: LIVER FIBROSIS IN HEPATITIS C VIRUS-INFECTED SUBJECTS,
TITLE OF INVENTION: METHODS OF DETECTION AND USES THEREOF
FILE REFERENCE: CL001469
FILE REFERENCE: CL001469
CURRENT APPLICATION NUMBER: US/60/487,610
CURRENT APPLICATION NUMBER: US/60/487,610
CURRENT FILING DATE: 2003-07-17
NUMBER OF SEQ ID NOS: 97101
SOFTWARE: FRATSEQ for Windows Version 4.0
SEQ ID NO 1384
LENGTH: 4989
TYPE: DNA
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Best Local S
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184; Conser
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              CTGGAGGGCGAGGACCGGGTATAAGAAGCCTCGTGGCCTTGCCCGGGCAGCCGCAGCTT 525
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llarity 47.8%;
Conservative
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Pred. No. 0.13;
D; Mismatches 197;
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                                                                                                                                                                                                                                                                                    6378
                                                                                                                                                                                                                                                                                                              550
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US-60-485-450-12047/c
; Sequence 12047, Appl
; GENERAL INFORMATION:
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APPLICANT: CARGILL, Michele
APPLICANT: CARGILL, Michele
APPLICANT: CARGILL, Michele
TITLE OF INVENTION: GENETIC POLYMORPHISMS ASSOCIATED WITH
TITLE OF INVENTION: RESPONSE TO INTERFERON TREATMENT IN HEPATITIS C
TITLE OF INVENTION: VIRUS-INFECTED SUBJECTS, METHODS OF DETECTION AND
TITLE OF INVENTION: THEREOF
FILE REFERENCE: CLOO1470
CURRENT APPLICATION NUMBER: US/60/485,450
CURRENT APPLICATION NUMBER: US/60/485,450
CURRENT FAILING DATE: 2003-07-09
NUMBER OF SEQ ID NOS: 47859
SOFTWARE: FRASESEQ FOR WINDOWS Version 4.0
SEQ ID NO 12047
LENGTH: 16525
TYPE: DNA
ORGANISM: Homo sapiens
US-60-485-450-12047
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Best Local Similarity
Matches 182; Conserv
                                                                                                                                                                                                                         Query Match 9.2
Best Local Similarity 48.8
Matches 163; Conservative
                                                                                                                                                              171 GAGGGAAGCTCCCTCACCNGAGGGAAGCTCCCCTCACCCGGCCCAGCCCTGCAGGGGGGG
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                                               CCCGGGCTCGGGCGCCGCCCCGGCCGGCCGGGCTGGGCCGCGCGAACGCATGGCCCG
                                                                GGC-CTCGCGGAGACAAAGGCCGGGCCTGCCTCTCTCAGAGGGGCCCCAGCGCCTGCCAAG
                                                                                                     CCTCGGCCGCAGCGGCCCCCAGGGCTCAGCGGGGCCCGGGGGGGCGCGGGGGC
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                                                                                                                                                                                                                         Score 50.6; DB 7;
Pred. No. 0.23;
0; Mismatches 170;
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RESULT 7
US-10-425-114A-2674/c
US-10-425-114A-2674, Application US/10425114A
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TITLE OF INVENTION: Nucleic Acid Molecules and Other Molecules Associated With TITLE OF INVENTION: Plants and Uses Thereof for Plant Improvement FILE REFERENCE: 38-21(5313)39 B CURRENT APPLICATION NUMBER: US/10/425,114A CURRENT FILING DATE: 2003-04-28 NUMBER OF SEQ ID NOS: 73128 SEQ ID NO 2674 LENGTH: 2368 TYPE: DNA ORGANISM: Zea mays ORGANISM: Zea mays
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Query Match 9.0%;
Best Local Similarity 45.0%;
Matches 224; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         APPLICANT: Liu, Jingdong APPLICANT: Zhou, Yihua
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Kovalic, David K.
Screen, Steven E
Tabaska, Jack E
                            GCCGCAGGTTCCCCCGCGC
                                                                                                   GAGGCCGGCGCTGGAGGGGCGAGGACCGGGTATAAGAAGCCTCGTGGCCTTGCCCGGGCA 515
                                                                                                                                        CGCCGCGGCGCGCGCGTCGACGAGCGCGCGCGCACGGAGGAGTCCGGGTCGCGGAC
                                                                                                                                                                                                                                                                                           CGAGGCCTCGACGGCGGCGGCGGCGAGCGCGGCGGCCAGCTGCGCGCACTGGTCCTG
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                                                                                                                                                                                                                 Yongwei
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Score 49.8; DB 6;
Pred. No. 0.25;
0; Mismatches 273;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 DB 6; Length 2368;
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; FERTURE:
; NAME/KEY: unsure
; LOCATION: (1)..(1215)
; OTHER INFORMATION: unsure at all n locations
US-09-897-516A-4197
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             APPLICANT: Goldman, Barry S.
APPLICANT: Hinkle, Gregory J.
APPLICANT: Hinkle, Gregory J.
APPLICANT: Hinkle, Gregory J.
APPLICANT: Malvar, Thomas M.
APPLICANT: Malvar, Thomas M.
APPLICANT: Slater, Steven C.
APPLICANT: Spiridonov, Sergei
TITLE OF INVENTION: Xenorhabdus sp. Genome SerilE REFERENCE: 38-21 (51847) B
CURRENT APPLICATION NUMBER: US/09/897,516A
CURRENT FILING DATE: 2001-06-39
PRIOR APPLICATION UNBER: US 60/215,161
PRIOR FILING DATE: 2000-06-30
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US-09-897-516A-4197/c
Commence 4197, Application US/09897516A
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PCT-US03-26780-822/c
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SEQUENCE 822, Application PC/TUS0326780

SEQUENCE 822, Application PC/TUS0326780

SEQUENCE 822, Application PC/TUS0326780

SEQUENCE 822, Application HURAN EDIXPERIDES ENCODED BY POLYNUCLEOTIDES AND METHODS OF TITLE OF INVENTION: HURAN POLYPERIDES ENCODED BY POLYNUCLEOTIDES AND METHODS OF TITLE OF INVENTION: HURAN POLYPERIDES

FILE REFERENCE: 08940.0014-00304

CURRENT APPLICATION NUMBER: PCT/US03/26780

CURRENT FILING DATE: 2002-08-29

PRIOR APPLICATION NUMBER: 60/406,519

PRIOR APPLICATION NUMBER: 60/406,559

PRIOR APPLICATION NUMBER: 60/406,655

PRIOR APPLICATION NUMBER: 60/406,655

PRIOR FILING DATE: 2002-08-29

PRIOR PRIOR PLING DATE: 2002-08-29

PRIOR PRIOR PLING DATE: 2002-08-29
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APPLICANT: Goldman, Barry S
APPLICANT: Hinkle, Gregory,
APPLICANT: Huesing, Joseph
APPLICANT: MALVAI, Thomas M
APPLICANT: MALVAI, Thomas M
APPLICANT: Krasomil-Osterfe
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SEQ ID NO 4197
LENGTH: 1215
TYPE: DNA
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Best Local
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ilarity 49.0%;
Conservative
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Pred. No. 0.25;
0; Mismatches 132;
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Qy Qy ρy DЬ QΥ

Вb Qy

FEATURE:

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PRIOR APPLICATION NUMBER: 60/406,642
PRIOR FILING DATE: 2002-08-29
PRIOR FILING DATE: 2002-08-29
PRIOR FILING DATE: 2002-08-29
PRIOR PELLING DATE: 2002-08-29
PRIOR PELLING DATE: 2002-08-29
PRIOR APPLICATION NUMBER: 60/406,576
PRIOR FILING DATE: 2002-08-29
PRIOR APPLICATION NUMBER: 60/406,646
PRIOR FILING DATE: 2002-08-29
PRIOR APPLICATION NUMBER: 60/406,666
PRIOR FILING DATE: 2002-08-29
PRIOR APPLICATION NUMBER: 60/406,653
PRIOR FILING DATE: 2002-08-29
PRIOR FILING DATE: 2002-08-29
PRIOR APPLICATION NUMBER: 60/406,653
PRIOR FILING DATE: 2002-08-29
PRIOR APPLICATION NUMBER: 60/406,653
PRIOR FILING DATE: 2002-08-29
PRIOR PILING DA
                                         RESULT 10
US-60-495-114-16671
Sequence 16671, Application US/60495114
Sequence 16671, Application US/60495114
GENERAL INFORMATION:
APPLICANT: CARGILL, Michele
TITLE OF INVENTION: POLYMORPHISMS IN NUCLEIC ACID MOLECULES
TITLE OF INVENTION: ENCODING HUMAN PROTEASE PROTEINS, METHODS OF DETECTION.
TITLE OF INVENTION: USES THEREOF
FILE REFERENCE: CL001480
CURRENT APPLICATION NUMBER: US/60/495,114
CURRENT FILING DATE: 2003-08-15
NUMBER OF SEQ ID NOS: 91238
SOFTWARE: FastSEQ for Windows Version 4.0
ENCTH: 65518
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ORGANISM: Homo sapiens
PCT-US03-26780-822
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Best Local Similarity
Matches 189; Conserv
ORGANISM: Homo sapiens
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pred. No. 0.31;
0; Mismatches 214;
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; FEATURE:
NAME/KEY: misc_feature
LOCATION: (1)...(65518)
OTHER INFORMATION: n =
US-60-495-114-16671
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US-60-495-114-16855
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Best Local S
Matches 107
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TITLE OF INVENTION: ENCODING HUMAN PROTEASE PROTEINS, METHODS
TITLE OF INVENTION: USES THEREOF
FILE REFERENCE: CL001480
CURRENT APPLICATION NUMBER: US/60/495,114
CURRENT FILING DATE: 2003-08-15
NUMBER OF SED ID NOS: 91238
SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 16855
LENGTH: 121612
TYPE: DNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Sequence 16855, Appl GENERAL INFORMATION: APPLICANT: CARGILL,
                                                                                                                                                                                                                                   Query Match 8.9%;
Best Local Similarity 52.5%;
Matches 107; Conservative
                                                                                                                                                                                                                                                                                                                                                                             ORGANISM: Homo sapiens
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107; Conserv
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CGCGGGGCGCGGGGGC 5992
                            GCAGGTTCCCCGCGCGCGCCCGAGC 542
                                                                                   GCCGGCGCTGGAGGGGCGAGGACCGGGTATAAGAAGCCTCGTGGCCTTGCCCCGGGCAGCC
                                                          Conservative
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                                                                                                                                                                                                                                              0;
                                                                                                                                                                                                                                          Score 48.8; DB 7;
Pred. No. 0.66;
0; Mismatches 97;
                                                                                                                                                                                                                                              97;
                                                                                                                                                                                                                                                                            Length 121612;
                                                                                                                                                                                                                                                 Indels
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RESULT 12 PCT-US03-11231-193/c

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; OTHER INFORMATION: Clone US-10-425-114A-26227
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US-10-425-114A-26227
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; ORGANISM: HSV2
PCT-US03-11231-193
                                                                   APPLICANT: Zhou, Yihua

APPLICANT: Kovalic, David K.

APPLICANT: Kovalic, David K.

APPLICANT: Screen, Steven E

APPLICANT: Tabaska, Jack E

APPLICANT: Tabaska, Jack E

APPLICANT: Cao, Yongwei

TITLE OF INVENTION: Nucleake Acid Molecules and Other Molecules Associated With

TITLE OF INVENTION: Plants and Uses Thereof for Plant Improvement

FILE REFERENCE: 38-21(53313)B

CURRENT APPLICATION NUMBER: US/10/425,114A

CURRENT APPLICATION NUMBER: US/10/425,114A

CURRENT FILING DATE: 2003-04-28

NUMBER OF SEO ID NOS: 7312B

SEO ID NO 2627

LENGTH: 2463

TYPE: DNA

ORGANISM: Homo sapiens
                                                                                                                                                                                                                                                                       Sequence 2627, Application US/10425114A
GENERAL INFORMATION:
APPLICANT: Liu, Jingdong
APPLICANT: Zhou, Yihua
     Query Match
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Best Local Similarity
Matches 157; Conserv
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SERERAL INFORMATION:
APPLICANT: Corixa Corporation
APPLICANT: Day, Craig H.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           APPLICANT: Hosker, Nancy A.
APPLICANT: Hosker, Nancy A.
APPLICANT: Parsons, Joseph M.
APPLICANT: Parsons, Joseph M.
TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE DIAGNOSIS AND
FILE REFERENCE: 210121,53801PC
CURRENT APPLICATION UNMERS: PCT/US03/11231
CURRENT FILING DATE: 2003-04-09
NUMBER OF SEQ ID NOS: 267
SOFTWARE: FastSEQ for Windows Version 4.0
TYPE: DNA
                                                            FEATURE:
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   18.6%;
                                             ID:
                                          LIB4118-190-H1_FLI
 Score 47.6;
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DB 6;
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Length 2463;
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APPLICANT: Zhou, Tihua
APPLICANT: Kovalic, David K.
APPLICANT: Screen, Steven E
APPLICANT: Tabaska, Jack E
APPLICANT: Tabaska, Jack E
ITILE OF INVENTION: Nucleic Acid Molecules and Other Molecules Associated With
ITILE OF INVENTION: Plants and Uses Thereof for Plant Improvement
FILE REFERENCE: 38-21(53313)B
CURRENT APPLICATION NUMBER: US/10/425,114A
CURRENT APPLICATION NUMBER: US/10/425,114A
CURRENT FILING DATE: 2003-04-28
SEQ ID NO 26232
LENGTH: 2475
TYPE: Nov.
                                                                                                                                                                                                                                                                                                                                                                                                                                        ; OTHER INFORMATION: Clone ID: LIB4119-019-H6_FLI US-10-425-114A-26232
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ORGANISM: Homo sapiens
                                                                                                                                                                                                                                                                                      243 TTCGCTCCGGGCTCGGAGCCTCCGAGGCCAGGCCAGTCCCCTGAGCCTTCGCCGGCCCCG
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140; Conserv
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                               CGTGGCCTTGCCCGGGCAGCCGCAGGTTCCCCGCGCGCCCCGAGCCCCCCGCGCC 551
                                                                   CGCCTGATGGACCTGGCTCCGGGCGGGCCGGGCCTGGCCGCCCCCTTGGGCC
                                                                                                        GECCCGCCGCCCAGCAGGAAGTTGGCCAGGGCACGGCCGTGAGCGGAGCGGGCAGGGC
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ilarity 47.6%;
Conservative
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0; Mismatches
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US-60-495-114-16806/c
US-60-495-114-16806/c
Sequence 16806, Application US/60495114

Sequence 16806, Application US/60495114

GENERAL INFORMATION:
GENERAL INFORMATION:
HITCH OF INVENTION: DOLYMORPHISMS IN NUCLEIC ACID MOLECULES
TITLE OF INVENTION: DESCRIBENCE FROTEINS, METHODS OF DETECTION AND
TITLE OF INVENTION: USES THEREOF
FILE REFERENCE: CL001480
CURRENT APPLICATION NUMBER: US/60/495,114
CURRENT FILING DATE: 2003-08-15
NUMBER OF SEQ ID NOS: 91238
SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 16806
LENGTH: 27991
TYPE: DNA
ORGANISM: Homo sapiens
FEATURE:
RAME/KEY: misc_feature
LOCATION: (1)...(27991)
COTHER INFORMATION: n = A,T,C or G, or insertion/deletion polymorphism (see Tables 1-
OTHER INFORMATION: n
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Search completed: September 20, 2003, 03:15:44
Job time: 116.54 secs
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Best Local Similarity 49.5%;
Matches 147; Conservative
                                                                        25458 CGCCCTCGCAGAACGCCGCGCGTCTTCCCGGGGCCTGGCGGGCCCGGGGACCGAGGGGGCC 25399
                                                                                                                                                                                                                                                                                                  25578 TCCACCGCCAGGCCCGGCAGGGGGGGGGGCCGGACCGCTCACGCCCGGCGTGCT 25519
                                                                                                                                                                                                                                                                                                                           264 CCGGGGTGGGCCTCGCGGAGACAAAGGCCGGGCCTGCCTCTCTCAGAGGGCCCCAGCGCC 323
                                                                                                                                                                                                                                                  204 TCACCCGGCCCAGCCCTGCAGGGGGGGGGGCGCGTGGGGGTCAGACCGCAAAGCGAAAGCTGCGGG 263
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Pred. No. 1.5;
0; Mismatches 149; Indels 1;
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Maximum Match 100%
Listing first 45 summaries
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Maximum DB
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                                                                              Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.
                                     Score
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312
1 atgaagctcgccgccctcct.....gggccctgacagtgtttggc 312
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                                                                                                                                                                                                                                                                                                                                                                                                                                              22781392 seqs, 12152238056 residues
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BI818715 603037535
                                      Description
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	52410	17.	707758 OV3-HT(02200 Ok69a06 s	6030376	19864 ns54a03.	7934 zd71b02.r1	049698 NISC	5414 zd61a04	12697 nx30g(a84h08	08998 603070	323159 60303	80649 UI-CF-	13307 UI-CF	UI-CF-	BM982112 UI-CF-	063a1	60303	F221778 7062e	744099 wc36c1	745557 463460	1919534 60303	20203 COINCET	11973/10 qp36d0	13337/0 gp98f0	BI400/00 000038866	1822360 60303	1819/95 60304	[819014 60303	[490604 60303	820788 60303	9045 60303	010	1/// UI-CE	TOTAL SEGRE	4/2/ ESISO	1524 AGENCE	006/624 AGENC	2000	1760700 6030850

BM920793

BM920793

TION AGENCOURT_6705937 NIH_MGC_115 Homo sapiens cDNA clone IMAGE:5752038

5', mRNA sequence.

BM920793

ION BM920793.1 GI:19371172

EST.

CHOMO sapiens (human)

HOMO sapiens (human)

HOMO sapiens (human)

HOMO sapiens (human)

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

MAMMALIA (Homo)

MAMALIA (Homo)

MAMMALIA (Homo)

MAMMALIA (Homo)

MAMMALIA (Homo)

ALIGNMENTS

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REFERENCE
AUTHORS
TITLE
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VERSION
KEYWORDS
SOURCE
ORGANISM
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BM920794
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Unpublished

Contact: Robert Strausberg, Ph.D.

Email: orgapbs remail.nih.gov

Tissue Procurement: Life Technologies, Inc.

CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)

DNA Sequencing by: Agencourt Bioscience Corporation

Clone distribution: MGC clone distribution information can
                                                                                                                                                            Homo sapiens (human)
Homo sapiens
Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Euthéria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 473)
NIH-MGC http://mgc.nci.nih.gov/.
National Institutes of Health, Mammalian Gene Collection (MGC)
                                                                                                                                                                                                                                                                                                                                473 bp

AGENCOURT_6705953 NIH_MGC_115 Homo

5', mRNA sequence.

BM920794

BM920794.1 GT:19371173
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//clope_libe_"NIH_MGC_115"
//note="Organ: pooled brain, lung, testis; Vector:
/note="Organ: pooled brain, lung, testis; Vector:
/note="Organ: pooled brain, lung, testis; Vector:
pCMV-SPORFG; Site_l: NotI; Site_2: EcoRV (destroyed); RNA
source anonymous pool of 6 male brains, age 69. Library is
oligo-dT primed and directionally cloned (EcoRV site is
destroyed upon cloning). Average insert size 11 & kb,
insert size range 1-3 kb .Library is normalized and enriched for full-length clones and was constructed by C.
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/clone="IMAGE:5752038"
/lab_host="DH10B"
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/mol_type="mRNA"
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Pred. No. 1.2e-50;
0; Mismatches 2;
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found through the I.M.A.G.E. Consortium/LLNL at:

http://image.llnl.gov
plate: LLAM12785 row: j column: 08

High quality sequence stop: 474.

Location/Qualifiers
1. 473

//OLTYPE-"MRNA"
//OLTYPE-"MRNA"
//OLONE_ILD-"NIH_MGC_115"
//LONE_ILD-"NIH_MGC_115"
//LONE_ILD-"NIH_MGC_INING. Age fange 23-27; 1
male lung, age 27; and 1 male testis, age 69. Library is
oligo-dT primed and directionally cloned (Ecorv Site is
destroyed upon cloning). Average insert size 1.8 kb,
insert size range 1-3 kb. Library is normalized and
enriched for full-length clones and was constructed by C.
Griber (Invitrogen). Research Genetics tracking code
Griber (Invitrogen). Research Genetics tracking code
Griber (Invitrogen). Research Genetics tracking code
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92 a 161 c 147 g 73 t

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GAGCTGGGTCCCCAGGCCGTGGGGGCCCTGAAGGCCCTGAAGGCCCTGCTGGGGGGCCCTG CTGAGCAGCCTGGGCATCCCCGTGAACCACCTCATAGAGGGCTCCCAGAAGTGTGTGGCT ACAGTGTTTGGC 312 99.0%; ilarity 99.4%; Conservative 318 ; Score 308.8; ; Pred. No. 1.2e 0; Mismatches ..2e-50; 2; Indels 0; Gaps 300 240 246 186 180 126 120 66 60

M977626/C

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M977626

UI-CF-ENI-aef-o-13-0-UI.sl UI-CF-ENI Homo sapiens cDNA clone
M977626

EXENCE

BM977626

BM977626

EXEMPLE Homo sapiens (human)

OURGANISM Homo sapiens (human)

OURGANISM Homo sapiens

EXEMPLE HOMO sapiens

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                                                                                                                                                                                                Email: paul-mocray@ulowa.edu
Tissue Procurement: Dr. M. J. Welsh, University of Towa
CDNA Library preparation: Dr. M. Bento Soares, University of Towa
CDNA Library Arrayed by: Dr. M. Bento Soares, University of Towa
CNA Sequencing by: Dr. M. Bento Soares, University of Towa
Clone Distribution: Researchers may obtain clones from Research
Genetics (www.resgen.com) or from Open Biosystems
(www.openbiosystems.com).
The following repetitive elements were found in this cDNA
sequence: 459-484, >GC_rich#Low_complexity
Seq primer: M13 FORMARD
POLYA-Yes.
                                               241
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Fax: 319 356 7171
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GAGCTGGGTCCCCAGGCCGTGGGGGCCCTGAAAGGCCCTGAAGGCCCTGCTGGGGGCCCTG
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ilarity 99.4%;
Conservative
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//clone_lib="UI-CF-EN1"
//clone_lib="UI-CF
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|mol_type="mRNA;
|db_xref="taxon:9606"
|/clone="UI-CF_ENI-aef-o-13-0-UI"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TAG_SEQ=CTGCTCAGGT"
154 c 175 g
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Bukaryota; Metazoa; Chordata; Catarrhini; Hominidae; Homo.

1 (bases 1 to 046)

25 1 (bases 1 to 046)

26 National Institutes of Health, Mammalian Gene Collection (MGC)

27 National Institutes of Health, Mammalian Gene Collection (MGC)

28 Null-MGC http://mgc.nci.nih.gov/.

29 National Institutes of Health, Mammalian Gene Collection (MGC)

20 Null-MGC Strausberg, Ph.D.

20 Email: cgapbs-r@mail.nih.gov

20 Email: cgapbs-r@mail.nih.gov

21 CDNA Library Preparation: Life Technologies, Inc.

21 CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LiNL)

21 DNA Sequencing by: Incyte Genomics, Inc.

22 Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LENL at:

23 Plate: LLAM11445 row: e column: 09

24 High quality sequence stop: 471.

25 Ince 1.486
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                                                                                                                                                                                                                                                                                                                                                                                                                        Conservative
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mol_type="mRNA"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           /clone_libe_NiH_MGC_115"
/clone_libe_NiH_MGC_115"
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/note="organ: pool of 6 male brains, age range 23-27; 1
source anonymous pool of 6 male brains, age 10 library is:
male lung, age 27; and 1 male testis, age 69 library is:
oligo-dT primed and directionally cloned (EcoRV site is:
oligo-dT primed and directionally cloned (EcoRV site is:
oligo-dT primed and directionally consent size 1 a kb,
destroyed upon cloning). Average insert size 1 a ld
insert size range 1-3 kb Library is normalized and
enriched for full-length clones and was constructed by C.
Gruber (Invitrogen). Research Genetics tracking code
021. Note: this is a NIH_MGC Library."

a 176 c 153 g 74 t
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Pred. No. 1.2e-50;
0; Mismatches 2;
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Matches 310
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ISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Eukaryota; Metazoa; Chordata; Catarrhini; Hominidae; Homo.

Primates; Catarrhini; Hominidae; Homo.

Nammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

RS NIH-MGC http://mgc.nci.nih.gov/.

RS NIH-MGC http://mgc.nci.nih.gov/.

National Institutes of Health, Mammalian Gene Collection (MGC)

Contact: Robert Strausberg, Ph.D.

Email: cgapbs-femail.nih.gov

Tissue Procurement: Life Technologies, Inc.

CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)

DNA Sequencing by: Incyte Genomics, Inc.

Clone distribution: MGC clone distribution information can be http://image.llnl.gov

plate: LLAMI1512 row: j column: 05

High quality sequence start: 3

High quality sequence stop: 416.

Location/Qualifiers
                      121 GAGGCCGGGGCCGGGACCCTGGCCAACCCCTCAACCCGCTGAACCCGCTGAAGCTCCTG
                                                                                                                                          83
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                                                                                                                                                                                                                                                   ATGAAGCTCGCCGCCCTCCTGGGGCTCTGCGTGGCCCTGTCCTGCAGCTCCGCTCCTGCT
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                                                                                                                                                                                                                                                                                                                                                                                                     Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     /note- organ: pooled lung and spleen; Vector: pCMV-SPORT6; Site_1: NotI; Site_2: EcoRV (destroyed); RNA source anonymous pool of 24 week female lung, 16 week female spleen, and 20-22 week male spleens. Library is oligo-dT primed and directionally cloned (EcoRV site is destroyed upon cloning). Average insert size 14 kb, insert size range 1-3 kb. Library is normalized and enriched for full-length clones and was constructed by C. Gruber (Invitrogen). Research Genetics tracking code 026. Note: this is a NIH_MGC Library."
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                                                                                                                                                                                                                                                                                                                                                                                                                            99.0%;
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                                                                                                                                                                                                                                                                                                                                                                                      Score 308.8; DB 12; Length 1004; Pred. No. 1.3e-50; 0; Mismatches 2; Indels 0;
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                                                                                                 61 TTCTTAGTGGGCTCGGCCAAGCCTGTGGCCCAGCCTGTCGCTGCGCTGGAGTCGGCGCG
                                                                                                                                                                                                                                    99.0%; Score 308.8; DB 13; 99.4%; Pred. No. 1.3e-50; 19.4%; Pred. No.
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Db	143 GAGGCCGGGGCCCGGGACCCTGGCCAACCCCCTCGGCACCCGCTGAAGCTCCTG 202
Qy	
Db	203 CTGAGCAGCCTGGGCATCCCCCTGAACCACCTCATAGAGGGCTCCCAGAAGTGTGTGT
Qy	241 GAGCTGGGTCCCCAGGCCGTGGGGGCCCTGAAGGCCCCTGCAGGCCCTGCTGGGGGCCCTG 300
Db	263 GAGCTGGGTCCCCAGGCCGTGGGGGCCCTGAAGGCCCTGAAGGCCCTGCTGGGGGCCCTG 322
Qy	301 ACAGTGTTTGGC 312
DЪ	323 ACAGTGTTTGGC 334
o a mode	
BQ067622	
DEFINITION	HQU67622 1059 bp mrNA linear EST 02-APR-2002 AGENCOURT_6759083 NIH_MGC_115 Homo sapiens cDNA clone IMAGE:5755192
ACCESSION	uence.
VERSION KEYWORDS	BQ067622.1 GI:19896668
SOURCE	Homo sapiens (human)
	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo
AUTHORS	I (bases 1 to 1059) NIH-MGC http://mgc.nci.nih.gov/
TITLE JOURNAL	National Institutes of Health, Mammalian Gene Collection (MGC)
COMMENT	Contact: Robert Strausberg, Ph.D.
	Tissue Procurement: Life Technologies, Inc. cDNA Library Preparation: Life Technologies, Inc. cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
	science Corporation stribution informat ortium/LLNL at:
FEATURES source	High quality sequence stop: 343. Location/Qualifiers 11059
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	/clone="IMAGE:5755192" /lab_host="DHIDB" /clone_lib="NIH_MGC_115"
	pCMV-SPORT6; Site_1: Not; Site_2: EcoRV (destroyed); RNA source anonymous pool of 6 male brains, age range 23-27; 1
	ed and directionally cloned on cloning). Average inserfange 1-3 kb. Library is norr full-length clones and was roden). Research Genetics is
BASE COUNT ORIGIN	NIH_MGC Library." 217 t
Query Match Best Local	Similarity
, to .	

Indels

0, Gaps

Query Ma Best Loc Matches Qy	BASE COUNT		FEATURES	REFERENCE AUTHORS TITLE JOURNAL COMMENT	LOCUS DEFINITION ACCESSION VERSION KEYWORDS SOURCE ORGANISM	Qy Db RESULT 7	Qy Db Qy	Oy Db
/ Match 99.0%; Score 308.8; DB 12; Length 1083; Local Similarity 99.4%; Pred. No. 1.3e-50; nes 310; Conservative 0; Mismatches 2; Indels 0; Gaps 0; 1 ATGAAGCTCGCCCCCCTGGGGCTCTGCGTGGCCCTGTCCTGCAGCTCCGCTGCT 60	212 8		Tissue Procedus Libsechus Libsechus Libsechus Libsechus Alberta del Clone diffound through the http://mmplate: LL High qual	Eukaryota; Met Mammalia; Euth 1 (bases 1 to NIH-MGC http:/ National Insti Unpublished Contact: Rober Email: cgapbs-	BM921624 1083 bp mRNA linear AGENCOURT_6707854 NIH_MGC_115 Homo sapiens cDNA clo 5', mRNA sequence. BM921624 BM921624 1 GI:19372003 EST. Sapiens (human) Homo sapiens (human)		181 CTGAGCAGCCTGGGCATCCCCGTGAACCACCTCATAGAGGGCTCCCAGAAGTGTGTGGCT 240	83 TICTTAGTGGGCTCGGCCAAGCCTGTGGCCCAGCCTGTCGCTGCGCTGGAGTCGGCGGCG 142 121 GAGGCCGGGGCCGGGACCCTGGCCAACCCCCTCGGCACCCTCAACCCGCTGAAGCTCCTG 180 111
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QY QY	Query Mat Best Loca Matches Qy	FEATURES SOUTO BASE COUNT ORIGIN	TITLE JOURNAL COMMENT	SOURCE ORGANISM REFERENCE AUTHORS	RESULT 8 AW974727 LOCUS DEFINITION ACCESSION VERSION KEYWORDS	Qy 2 pb 2 Qy 3 pb 3	Qy 1: Db 1: Qy 1 Db 2	Ωb
61 TCTTAGTGGCTCGCCAAGCCTGTGCCCAAGCCTGCCGCTGCGCTGGAGTCGGCGGGGGGGG	1 1 2 2 5 2 5	Location/Qual 1	Assessment of gene expression patterns metastasis using a 19,200 element cDNA Unpublished Contact: John Quackenbush The Institute for Genomic Research 9712 Medical Center Dr., Rockville, MD 7712 Medical Center Dr., Rockville, MD 781: 301 838 3528 Fax: 301 838 3208 Email: johng@tigr.org	uman zoa; ria; 550) Ak	AW974727 EST386817 MAGE resequences, MAGN Homo sapiens AW974727 AW974727 EST 4727.1 GI:8165915	241 GAGCTGGGTCCCCAGGCCGTGGGGGCCGTGAAGGCCCTGCTGGGGGCCCTG	21 61 81 21	41 ATGAAGCTCGCCGCCCTCCTGGGGCTCTGCGTGCCCTGTCCTGCAGCTCCGCTGCTGCTGCAGCTCCGCGCGCG

129

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309

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                                                                                                      Similarity
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                      GCTCGCCGCCTQCTGGGGCTCTGCGTGGCCCTGTCCTGCAGCTCCGCTCGTGCTTTCTT 65
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Homo sapiens (human)
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                                                                                        Conservative
                                                                                                                                                                   63
                                                                                                                                                      /note="Organ: prostate; vector: pT7T3D-Pac (Pharmacia)
/note="Organ: prostate; vector: pT7T3D-Pac (Pharmacia)
with a modified polylinker; plasmid DNA from the
normalized library NCT_CGAP_Pr22 was prepared, and ss
circles were made in vitro. Following HAP purification,
this DNA was used as tracer in a subtractive hybridization
reaction. The driver was PCR-amplified cDNAs from a pool
of 5,000 clones made from the same library (cloneIDs
985608-986759, 1101192-1101959, and 1217928-1220615).
Subtraction by Bento Scares and M. Fatima Bonaldo. "
a 158 c 145 g 71 t
                                                                                                                                                                                                                                                                                                                                                                         /organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/clone="IMAGE:3271401"
                                                                                                                                                                                                                                                                                                            /lab_host="DH10B"
/clone_lib="NCI_CGAP_Pr28"
                                                                                                                                                                                                                                                                                                                                                              /sex="male"
                                                                                                                                                                                                                                                                                                                                                'dev_stage="adult"
                                                                                                     97.4%;
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                                                                                       0;
                                                                                   Score 303.8; DB 14;
Pred. No. 1.1e-49;
0; Mismatches 2;
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                                                                                                                                                                                                                                                                     Email: paul-mccray@uiowa.edu
Tissue Procurement: Dr. M. J. Welsh, University of Iowa
cDNA Library preparation: Dr. M. Bento Soares, University
cDNA Library Arrayed by: Dr. M. Bento Soares, University of
DNA Sequencing by: Dr. M. Bento Soares, University of Iowa
Clone Distribution: Researchers may obtain clones from Res
Genetics (www.resgen.com) or from Open Biosystems
(www.openblosystems.com).
Seq primer: M13 FORWARD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo. 1 (bases 1 to 472) Bonaldo, M.F., Lennon, G. and Soares, M.B. Normalization and subtraction: two approaches to facilitate gene discovery
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                                                                                                                                                                                                                                                                                                                                                                                                             2024 University of Iowa Med Labs, Iowa City, Tel: 319 356 4866 Fax: 319 356 7171
                                                                                                                                                                                                                                                           POLYA=Yes
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Contact: McCray, PB
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Genome Res. 6 (9), 791-806 (1996)
97044477
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              BM977779 A72 bp mRNA linear UI-CF-EN1-aef-n-17-0-UI.slUI-CF-EN1 Homo sapiens UI-CF-EN1-aef-n-17-0-UI 3', mRNA sequence. BM977779 BM977779.1 GI:19596542
                                                                                                                                                                                                                                                                                                                                                                                                                                                       University of Iowa
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Homo sapiens
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/dev_stage="Adult"
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/lab_host="BH10B (Life Technologies) (T1 phage resistant)"
/clone_lib="UI_CF_ENI"
/clone_lib="UI_CF_ENI"
/note="Organ: Lung; Vector: pT7T3-Pac (Pharmacia) with a
modified polylinker; Site_1: Ecor ; Site_2: Not 1;
UI-CF-ENI is a normalized cDNA library containing the
following tissue(s): Primary Lung Cystlo Fibrosis
Epithelial Cells. The library was constructed according to
Bonaldo, Lennon and Soares, Genome Research, 6:791-806,
                                                                                                                                        /tissue_type="Primary Lung
Cells"
                                                                                                                                                                  /organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/clone="UI-CF-EN1-aef-n-17-0-UI"
                                                                                                                                                                                                                                           location/Qualifiers
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                                                                                                                                                  Cystic Fibrosis Epithelial
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EST 21-FEB-2003 CDNA clone

Research of

Iowa

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AI685860
                                                                                                                                                                                                                                                                                                                                                                                                                      AI685860
tt90f09.x1 NCI_CGAP_Pr28
Contact: Robert Strausberg, Ph.D.

Contact: Robert Strausberg, Ph.D.

Emmail: Grapbs-remail.nih.gov

Tissue Procurement: Michael J. Brownstein, M.D., Ph.D., Michael R.

Emmert-Buck, M.D., Ph.D.

CDNA Library Preparation: M. Bento Soares, Ph.D.

CDNA Library Preparation: M. Bento Soares, Ph.D.

CDNA Library Arrayed by: Greg Lennon, Ph.D.

DNA Sequencing by: Washington University Genome Sequencing Center

DNA Sequencing by: Washington University Genome Acquencing Center

Clone distribution: NCI-CGAP clone distribution information can be
found through the I.M.A.G.E. Consortium/LLNL at:

www-bio.llni.gov/bbrp/image/image.html

Seq primer: -40Up from Gibco.

Location/Qualifiers
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Mammalia; Eutheria; Primates; Catarrhini; Hominid
1 (bases 1 to 439)
NCI-CGAP http://www.ncbi.nlm.nih.gov/ncicgap.
National Cancer Institute, Cancer Genome Anatomy
                                                                                                                                                                                                                                                                                                                                                                       AI685860.1 GI:4897154
                                                                                                                                                                                                                                                                                                                     Homo sapiens (human)
                                                                                                                                                                                                     Unpublished
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TAG_SEQ=CTGCTCAGGT"
a 148 c 158 g
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TAG_TISSUE-Human Lung Epithelial Cell Lines untreated LPS
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Pred. No. 6.
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Homo sapiens (human)
Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Eukaryota; Metazoa; Chordata; Catarrhini; Hominidae; Homo.
Mammalla; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 961)
NIH-MGC http://mgc.nci.nih.gov/.
National Institutes of Health, Mammalian Gene Collection (MGC)
National Institutes of Health, Mammalian Gene Collection, (Positional Institutes of Health, Mammalian Gene Collection, (Positional Institutes), Ph.D.

Email: cgapbs-remail.nih.gov

Tissue Procurement: Life Technologies, Inc.
cDNA Library Preparation: Life Technologies, Inc.
cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
cDNA Sequencing by: Incyte Genomics, Inc.
clone distribution: MGC clone distribution information can
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       mRNA sequence.
BI819045
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603033186F1 NIH_MGC_115
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                /clone_libs" NCI_CGAP_Pr28"
/clone_libs" NCI_CGAP_Pr28"
/clone_libs" NCI_CGAP_Pr28
/clone_libs" NCI_CGAP_Pr28
/clores Normalized library NCI_CGAP_Pr22 was prepared, and ss normalized library NCI_CGAP_Pr22 was prepared, and ss circles were made in vitro. Following HAP purification, this DNA was used as tracer in a subtractive hybridization this DNA was used as tracer in a subtractive hybridization of 5,000 clones made from the same library (cloneIDs 98508-986759, 1101192-1101959, and 1217928-1220615).
Subtraction by Bento Soares and M. Fatima Bonaldo. "a 140 c 155 g 73 t
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/lab_host="DH10B"
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Pred. No. 1e-48;
0; Mismatches 2;
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Homo sapiens cDNA clone IMAGE:5174540 5',
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                                                                                                                                                                                                                                                                                                                                                                                                                                             BI820788 407 bp mRNA linear 603034390F1 NIH_MGC_115 Homo sapiens cDNA clone IMA mRNA sequence.
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Unpublished Contact: Robert Strausberg, Ph.D Email: cgapbs-r@mail.nih.gov
                                                                                                                                                                                   Homo sapiens (human)
Homo sapiens
Eukaryota, Metazoa; Chordata;
Mammalia; Eutheria; Primates;
1 (bases 1 to 407)
                                                                                                        NIH-MGC http://mgc.nci.nih.gov/.
                                                                                                                                                                                                                                                                                                                                                                                                                BI820788.1 GI:15932338
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TRANCTRONGTOCCCANGCCGTGGGGGGCCCTGAAGGCCCTGAAGGCCCTGCTGGGGGCCCTCTTGGGGGCCCTGAAGGCCCTGAAGGCCCTGAAGGCCCTGCTGGGGGCCCTTGAAGGCCCTGAAGGCCCTGCTGGTGGGGGCCCTTGAAGGCCCTGAAGGCCCTTGAAGGCCCTTGAAGGCCCTTGAAGGCCCTTGAAGGCCCTTGAAGGCCCTTGAAGGCCCTTGAAGGCCCTTGAAGGCCCTTGAAGGCCCTTGAAGGCCCTTGAAGGCCCTTGAAGGCCCTTGAAGGCCCTTGAAGGCCCTTGAAGGCCCTTGAAGGCCCTTGAAGGCCCTTGAAGGCCCTTGAAGGCCCTTGAAGGCCCTTGAAGGCCCTTGAAGGCCCTTGAAGGCCCTTGAAGGCCCTTGAAGGCCCTTGAAGGCCCTTGAAGGCCCTTGAAGGCCCTTGAAGGCCCTTGAAGGCCCTTGAAGGCCCTTGAAGGCCCTTGAAGGCCCTTGAAGGCCCTTGAAGGCCCTTGAAGGCCCTTGAAGGCCCTTGAAGGCCCTTGAAGGCCCTTGAAGGCCCTTGAAGGCCCTTGAAGGCCCTTGAAGGCCCTTGAAGGCCCTTGAAGGCCCTTGAAGGCCCTTGAAGGCCCTTGAAGGCCCTTGAAGGCCCTTGAAGGCCCTTGAAGGCCCTTGAAGGCCCTTGAAGGCCCTTGAAGGCCCTTGAAGGCCCTTGAAGGCCCTTGAAGGCCCTTGAAGGCCCTTGAAGGCCCTTGAAGGCCCTTGAAGGCCCTTGAAGGCCCTTGAAGGCCCTTGAAGGCCCTTGAAGGCCCTTGAAGGCCCTTGAAGGCCCTTGAAGGCCCTTGAAGGCCCTTGAAGGCCCTTGAAGGCCCTTGAAGGCCCTTGAAGGCCCTTGAAGGCCCTTGAAGGCCCTTGAAGGCCCTTGAAGGCCCTTGAAGGCCCTTGAAGGCCCTTGAAGGCCCTTGAAGGCCCTTGAAGGCCCTTGAAGGCCCTTGAAGGCCCTTGAAGGCCCTTGAAGGCCCTTGAAGGCCCTTGAAGGCCCTTGAAGGCCCTTGAAGGCCCTTGAAGGCCCTTGAAGGCCCTTGAAGGCCCTTGAAGGCCCTTGAAGGCCCTTGAAGGCCCTTGAAGGCCCTTGAAGGCCCTTGAAGGCCCTTGAAGGCCCTTGAAGGCCCTTGAAGGCCCTTGAAGGCCCTTGAAGGCCCTTGAAGGCCCTTGAAGGCCCTTGAAGGCCCTTGAAGGCCCTTGAAGGCCCTTGAAGGCCCTTGAAGGCCCTTGAAGGCCCTTGAAGGCCCTTGAAGGCCCTTGAAGGCCCTTGAAGGCCCTTGAAGGCCCTTGAAGGCCCTTGAAGGCCCTTGAAGGCCCTTGAAGGCCCTTGAAGGCCCTTGAAGGCCCTTGAAGGCCCTTGAAGGCCCTTGAAGGCCCTTGAAGGCCCTTGAAGGCCCTTGAAGGCCCTTGAAGGCCCTTGAAGGCCCTTGAAGGCCCTTGAAGGCCCTTGAAGGCCCTTGAAGGCCCTTGAAGGCCCTTGAAGGCCCTTGAAGGCCCTTGAAGGCCCTTGAAGGCCCTTGAAGGCCCTTGAAGGCCCTTGAAGGCCCTTGAAGGCCCTTGAAGGCCCTTGAAGGCCCTTGAAGGCCCTTGAAGGCCCTTGAAGGCCCTTGAAGGCCCTTGAAGGCCCTTGAAGGCCCTTGAAGGCCCTTGAAGGCCCTTGAAGGCCCTTGAAGGCCCTTGAAGGCCCTTGAAGGCCCTTGAAGGCCCTTGAAGGCCCTTGAAGGCCCTTGAAGGCCCTTGAAGGCCCTTGAAGGCCCTTGAAGGCCCTTGAAGGCCCTTGAAGGCCCTTGAAGGCCCTTGAAGGCCCTTGAAGGCCCTTGAAGGCCCTTGAAGGCCCTTGAAGGCCCTTGAAGGCCCTTGAAGGCCCTTGAAGGCCCTTGAAGGCCCTTGAAGGCCCTTGAAGGCCCTTGAAGGCCCTTGAAGGCCCTTGAAGAAGGCCCTTGAAGGCCCTTGAAGGCCCTTGAAGGCCCTTGAAGGCCCTTGAAGGCCCTTGAAGGC
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//organism="Homo sapiens"
//organism="MANA"
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/lab_host="DH10B"
//lab_host="DH10B"
//olone="Tygan: pooled brain, lung, testis; Vector:
//orea="Organ: pooled brain, lung, testis; Vector: pooled brain, lung, testis; Vector:
//orea="Organ: pooled brain, lung, testis; Vector: pooled brain, lung, testis; Ve
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pred. No. 1.7e-48;
0; Mismatches 2;
                                                                                                                                                                                                                        Craniata; Vertebrata; Euteleostomi; Catarrhini; Hominidae; Homo.
                                                                                                                Mammalian
                                                                                                                Gene Collection (MGC
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                                                                                                                                                                               ACCESSION
VERSION
KEYWORDS
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BI490604/c
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Best Local
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241 GAGCTGGGTCCCCAGGCCGTGGGGGCCCTGAAGGCCCTGCAGGCCCTGCTGGGGGGCCCTG 300
247 GAGCTGGGTCCCCAGGCCGTGGGGGCCCTGAAGGCCCTGAAGGCCCTGCTGGGGGCCCTG 306
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        121 GAGGCCGGGGCCGGGACCCTGGCCAACCCCCTCGGCACCCTCAACCCGCTGAAGCTCCTG 180
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cDNA Library Preparation: Life Technologies, Inc.
cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Incyte Genomics, Inc.
Clone distribution: MGC clone distribution information can
found through the I.M.A.G.E. Consortium/LLNL at:
http://image.llnl.gov
plate: LLAN11437 row: c column: 23
High quality sequence start: 4
High quality sequence stop: 405.
Location/Qualifiers
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo. 1 (bases 1 to 416)
                                                                                                                           Homo sapiens (human)
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                                                                                                                                                                                                                                                                                                                                           mRNA sequence.
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603032283T1 NIH_MGC_115
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09; Conservative
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/clone="IMAGE:5175502"
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Pred. No. 2.56
0; Mismatches
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Homo
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les 2;
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ACCESSION
VERSION
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                                                                                  RESULT 15
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BIB19014
603033130F1 NIH_MGC_115 H
mRNA sequence:
BIB19014
BIB19014.1 GI:15930564
EST.
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National Institutes of Health, Mammalian Gene Collection (MGC)
Unpublished
Contact: Robert Strausberg, Ph.D.
Email: cgapbs-r@mail.nih.gov
Tissue Procurement: Life Technologies, Inc.
cDNA Library Preparation: Life Technologies, Inc.
cDNA Library Preparation: Life Technologies, Inc.
cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Incyte Genomics, Inc.
Clone distribution: MGC clone distribution information can be
found through the I.M.A.G.E. Consortium/LLNL at:
http://lmage.llnl.gov
Plate: LLAM11431 row: f column: 21
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    High quality sequence start: 6
High quality sequence stop: 416.
Location/Qualifiers
                                                                                                                                                            GAGCTGGGTCCCCAGGCCGTGGGGGGCCGTGAAGGCCCTGAAGGCCCTGCTGGGGGGCCCTG 300
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          /clone_lib="NIH_MGC_115"
/clone_lib="NIH_MGC_115"
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/note="Organ: pooled brain, lung, testis; Vector:
/note="Organ: pool of 5 male brains, age range 23-27; 1
male lung, age 27; and 1 male testis, age 69. Library is
oligo-dr primed and directionally cloned (EcoRv site is
destroyed upon cloning). Average insert size 18 kb,
insert size range 1-3 kb. Library is normalized and
enriched for full-length clones and was constructed by C.
Gruber (Invitrogen). Research Genetics tracking code
o21. Note: this is a NIH_MGC Library."
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         /db_xref="taxon:9606"
/clone="IMAGE:5173268"
/lab_host="DH10B"
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/mol_type="mRNA"
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Pred. No. 2.5e-48;
0; Mismatches 2; Indels 1;
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Homo
                                                               sapiens
                                                                 mRNA linea
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Search completed: September 20, Job time: 1390.21 secs
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Email: cgapbs-r@mail.nih.gov
Tissue Procurement: Life Technologies,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               CDNA Library Preparation: Life Technologies, Inc.
CDNA Library Arrayed by: The I.M.A.G.E. Consortium
CDNA Sequencing by: Incyte Genomics, Inc.
Clone distribution: MGC clone distribution information can be
found through the I.M.A.G.E. Consortium/LLNL at:
http://image.llnl.gov
Plate: LLANAl1434 row: k column: 07
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NIH-MGC http://mgc.nci.nih.gov/.
National Institutes of Health, Mammalian Gene Collection (MGC)
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APPLICANT: Baker, Kevin P.
APPLICANT: Botstein, David
APPLICANT: Desnoyers, Luc
APPLICANT: Eaton, Dan L.
APPLICANT: Ferrara, Mapoleone
APPLICANT: Fong, Sherman
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Goddard, Audrey
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US-09-120-878-19

US-09-141-908-1

US-09-155-9410-19

US-09-252-991A-6631

US-09-252-991A-6633

US-09-252-991A-6761

US-09-252-991A-6761

US-09-252-991A-6761

US-09-252-991A-7865

US-08-845-998-7

US-08-845-998-7

US-09-252-991A-7812

US-09-252-991A-7812

US-09-252-991A-7601

US-09-252-991A-7601
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Result No.

Score

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Minimum Maximum

DB seq

Database

Title: Perfect score: Sequence:

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Scoring table:

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: 1998-06-26 NUMBER: 60/0913 : 1998-07-01 NUMBER: 60/0914 NUMBER: 60/0915 : 1998-07-02 : 1998-07-02 NUMBER: 60/0916 : 1998-07-02 NUMBER: 60/0916 NUMBER: 60/0916 NUMBER: 60/0916 NUMBER: 60/0916	INDEER: 60/090	I 198-06-1998 I 1998-06-299 I	:: 1998-06-17 NUMBER: 60/08 : 1998-06-17 NUMBER: 60/08 1 1998-06-18 NUMBER: 60/08 1 1998-06-18 NUMBER: 60/08 1 1998-06-18 NUMBER: 60/08 1 1998-06-19 NUMBER: 60/08 1 1998-06-19 NUMBER: 60/08
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PRIOR APPLICATION NUMBER: 60/084600
PRIOR FILING DATE: 1998-05-07
PRIOR APPLICATION NUMBER: 60/087016
PRIOR APPLICATION NUMBER: 60/087609
PRIOR FILING DATE: 1998-06-02
PRIOR APPLICATION NUMBER: 60/087609
PRIOR FILING DATE: 1998-06-02
PRIOR APPLICATION NUMBER: 60/087609
PRIOR PRIOR APPLICATION NUMBER: 60/080021
PRIOR APPLICATION NUMBER: 60/080020
PRIOR FILING DATE: 1998-06-04
PRIOR APPLICATION NUMBER: 60/08003
PRIOR PRIOR APPLICATION NUMBER: 60/08003
PRIOR FILING DATE: 1998-06-04
PRIOR APPLICATION NUMBER: 60/08003
PRIOR PRIOR APPLICATION NUMBER: 60/08003
PRIOR APPLICATION NUMBER: 60/080202
PRIOR PRIOR APPLICATION NUMBER: 60/080202
PRIOR APPLICATION NUMBER: 60/0808010
PRIOR APPLICATION NUMBER

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Sequence 2, Application US/08964725

Patent No. 5939265

GENERAL IMPORMATION:
COHEN, Maurice
APPLICANY: COHEN, Maurice
APPLICANY: GONDON, Julian
APPLICANY: GONDON, Julian
APPLICANY: KIASS, Michael R.
APPLICANY: KRATOCHYLL, Jon D.
APPLICANY: KRATOCHYLL, John C.
APPLICANY: ROBERTS-RAPP, Lisa
APPLICANY: ROBERTS-RAPP, Lisa
APPLICANY: STROUPE, Steven D.
TITLE OF INVENTION: REACENTS AND METHODS USEFUL
TITLE OF INVENTION: FOR DETECTING DISEASES OF THE LUNG
NUMBER OF SEQUENCES: 19
CORRESPONDENCE ADDRESS:
ADDRESSEE: ADDRESS:
ADDRESSEE: ADBOTT LABOTATORIES
STREET: 100 Abbott Park
COINMAND: IL
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US-08-964-725-2
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PRIOR FILING DATE: 1998-07-07
PRIOR APPLICATION NUMBER: 60/091982
PRIOR FILING DATE: 1998-07-07
PRIOR APPLICATION NUMBER: 60/092182
PRIOR FILING DATE: 1998-07-09
                                                           COUNTRY: USA
ZIP: 60064-3500
ZIP: 60064-3500
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
COMPUTER: IBM Compatible
OPERATING SYSTEM: DOS
SOFTWARE: FastEEQ for Windows Version 2.
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/964,725
FILING DATE:
FILING DATE:
                    CLASSIFICATION: 435
PRIOR APPLICATION NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Local
ATTORNEY/AGENT INFORMATION
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10; Conservative
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17-07
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Pred. No. 3e-53;
0; Mismatches 2;
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Sequence 4, Application US/08964725

patent No. 5939265

patent No. 5939265

GENERAL INFORMATION:
GENERAL INFORMATION:
APPLICANT: FRIEDMAN, Paula N.
APPLICANT: HODGES, Steven C.
APPLICANT: KLASS, Michael R.
APPLICANT: KLASS, Michael R.
APPLICANT: KRATOCHYLI, Jon D.
APPLICANT: ROBERTS-RAPP, Lisa
APPLICANT: ROBERTS-RAPP, Lisa
APPLICANT: RUSSELL, John C.
APPLICANT: RUSSELL, John C.
APPLICANT: STROUPE, Steven D.
APPLICANT: RUSSELL, John C.
ITITLE OF INVENTION: FOR DETECTING DISEASES OF THE LUNG
TITLE OF INVENTION: FOR DETECTING DISEASES OF THE LUNG
STREET: 100 Abbott Dark Road
CITY: Abbott Park Road
CTITY: Abbott Park
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ; STRANDEDNESS:
; TOPOLOGY: lir
US-08-964-725-2
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US-08-964-725-4
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Best Local
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
LENGTH: 263 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
                                                                                                           STATE: ILL
COUNTRY: USA
ZIP: 60064-3500
ZIP: 60064-3500
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
COMPUTER: IBM Compatible
OPERATING SYSTEM: DOS
OPERATING SYSTEM: DOS
SOFTWARE: FastSEO for Windows Version 2.
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/964,725
EILING DATE: US/08/964,725
PRIOR APPLICATION DATA:
APPLICATION NUMBER:
EILING DATE: APPLICATION DATA:
APPLICATION NUMBER:
EILING DATE: APPLICATION DATA:
APPLICATION NUMBER:
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REGISTRATION NUMBER: 35,441
REFERENCE/DOCKET NUMBER: 59;
TELECOMMUNICATION INFORMATION:
TELEPHONE: 847/935-1729
TELEFAX: 847/938-2623
ATTORNEY AGENT INFORMATION:
NAME: Becker, Cheryl L.
REGISTRATION NUMBER: 35,441
REFERENCE/DOCKET NUMBER: 59
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            137 CCCTGGCCAACCCCTCGGCACCCTCAACCCGGTGAAGCTCCTGCTGAGCAGCCTGGGCA 196
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                120 TTTCTGTTGAGCACCTTGTGGAGGGGCTAAGGAAGTGTGTAAATGAGCTGGGACCAGAGG
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5. 5939265
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93; Conserv
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Pred. No. 0.0026;
0; Mismatches
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                           5997.US.P1
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Gaps

256 327

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Sequence 5, Application US/08964725 Patent No. 5939265
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                                                 APPLICATION UMBER: US/08/964
FILING DATE:
CLASSIFICATION: 435
PRIOR APPLICATION UMBER:
APPLICATION NUMBER:
FILING DATE:
APPLICATION NUMBER:
FILING DATE:
APPLICATION NUMBER:
AFTORNEY/AGENT INFORMATION:
NAME: Becker, Cheryl L.
REGISTRATION NUMBER: 35,441
REGISTRATION NUMBER: 5997
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
  TELEX:
INFORMATION FOR SEQ ID
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
LENGTH: 507 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
                                                                                                                                                                                                                                                                 COMPUTER: IBM Compatible
OPERATING SYSTEM: DOS
SOFTWARE: FastSEQ for Windows Version
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                            COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
                                                                                                                                                                                                                                                                                                                                                                                                                                   CORRESPONDENCE ADDRESS:
ADDRESSEE: Abbott Laboratories
STREET: 100 Abbott Park Road
CITY: Abbott Park
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          APPLICANT: STROUPE, TITLE OF INVENTION: TITLE OF INVENTION: NUMBER OF SEQUENCES:
                                                                                                                                                                                                                                                                                                                                                                                 COUNTRY: USA
ZIP: 60064-3500
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TOPOLOGY: linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TELEPHONE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TT: GORDON, JUlian
TT: HODGES, Steven C.
TT: KLASS, Michael R.
TT: KRATOCHVIL, Jon D.
TT: KRATOCHVIL, Jon D.
TT: ROSERTS-RAPP, Lisa
TT: RUSSELL, John C.
TT: STROUPE, Steven D.
TINVENTION: REAGENTS AND METHODS USEFUL
INVENTION: FOR DETECTING DISEASES OF THE LUNG
F SEQUENCES: 19
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   CCGTGGGGGCCGTGAAGGCCCTGCT 290
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                                       847/938-2623
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847/938†2623
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      o
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                                                                                                                                                                                                                                                       US/08/964,725
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                                                                                                                                                                                                                                              APPLICANT: DIMMARC, Radoje T.

APPLICANT: DIMMARC, Radoje T.

TITLE OF INVENTION: No. 656962e1 Nucleic Acids and

TITLE OF INVENTION: Polypeptides

FILE REFERENCE: 784C1P2B

CURRENT APPLICATION NUMBER: US/09/620,312D

CURRENT FILING DATE: 2000-07-19

PRIOR APPLICATION NUMBER: 09/52,317

PRIOR TILING DATE: 2000-04-25

PRIOR TILING DATE: 2000-04-25

PRIOR APPLICATION NUMBER: 09/488,725

PRIOR APPLICATION NUMBER: 09/488,725

PRIOR FILING DATE: 2000-01-21

NUMBER OF SEQ ID NOS: 1105

SEQ ID NO 47

LENGTH: 2497
                                                                      ; NAME/KEY: misc_feature; LCCATION: (1)...(2497); OTHER INFORMATION: n = a,t,c US-09-620-312D-47
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US-09-620-312D-47
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TOPOLOGY: US-08-964-725-5
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Best Local S
Matches 93
Query Match 15.8
Best Local Similarity 50.0
Matches 151; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Patent No.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             APPLICANT:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      APPLICANT
                                                                                                                                                                                                 TYPE: DNA
ORGANISM: Homo sapiens
FEATURE:
                                                                                                                                               NAME/KEY: CDS
LOCATION: (107)..(1756)
FEATURE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SEQUENCE CHARACTERISTICS:
LENGTH: 519 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                328 CTTCTGAAGCTGTGAAGAAACTGCTGGAGGCGCT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           257 CCGTGGGGGCCGTGAAGGCCCTGCT 290
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                INFORMATION:
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o. 6569662
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Similarity 60.4%;
93; Conservative
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Yang, Yonghong
Yang, Yonghong
Wang, Jian-Rui
Zhou, Ping
Ma, Yunging
Ma, Yunging
Wang, Dunrui
Wang, Zhiwei
John Tillinghast
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Chen, Rui-hong
Zhao, Qing A.
Wehrman, Tom
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Asundi, Vinod
Zhang, Jie
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  Score 49.2; DB 4;
Pred. No. 0.068;
0; Mismatches 148;
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TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PSEUDOMONAS TITLE OF INVENTION: AERUGINOSA FOR DIAGNOSTICS AND THERAPEUTICS: FILE REFERENCE: 107195.136
CURRENT APPLICATION NUMBER: US/09/252,991A
CURRENT FILING DATE: 1999-02-18
PRIOR APPLICATION NUMBER: US 60/074,788
PRIOR APPLICATION NUMBER: US 60/074,788
PRIOR FILING DATE: 1998-02-18
PRIOR APPLICATION NUMBER: US 60/094,190
PRIOR APPLICATION NUMBER: US 60/094,190
LENGTH: 2274
TYPE: DNa
RESULT 7
US-09-252-991A-3615
; Sequence 3615, Application US/09252991A
; Patent No. 6551795
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US-09-252-991A-3660
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                                                                                                                                                                                                                                                                                                                            Query Match 14.9%;
Best Local Similarity 51.2%;
Matches 109; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                   TYPE: DNA
ORGANISM: Pseudomonas aeruginosa
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                1219
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                                                                                                                                                                                                                                                                                                                          Score 46.6; DB 4; Length 2274; Pred. No. 0.22; 0; Mismatches 104; Indels 0
                                                                                                                                                                                                                                                                                                                            0;
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Best Local :
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                                                                                                                                                            Query Match
                                                                       408 CGCGGTGGGCACCGGGCTCAACGCGCCGAAGGGCTTCGCCGACGCCATCGCCGAAAT
                                       Similarity
                                                                                                    CGCCGCCCTCCTGGGGCTCTGCGTGCCTGTCCTGCAGCTCCGCTCGTGCTTTCTTAGT 68
                                                                                                                                  Conservative
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NUMBER OF SEQ ID NOS: 33142
; SEQ ID NO 3615
; LENGTH: 3297
; TYPE: DNA
; ORGANISM: Pseudomonas aeruginosa
US-09-252-991A-3615
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APPLICANT: MATC J. Rubenfield et al.
APPLICANT: MATC J. Rubenfield et al.
APPLICANT: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PSEUDOMONAS
TITLE OF INVENTION: AERUGINOSA FOR DIAGNOSTICS AND THERAPEUTICS
FILE REFERENCE: 107196.136
CURRENT APPLICATION NUMBER: US/09/252,991A
CURRENT FILING DATE: 1999-02-18
PRIOR APPLICATION NUMBER: US 60/074,788
PRIOR APPLICATION NUMBER: US 60/074,788
PRIOR APPLICATION NUMBER: US 60/094,190
PRIOR FILING DATE: 1998-07-27
PRIOR FILING DATE: 1998-07-27
                                                                                                                                                                                                                                                                                                                                                                                                     Local Similarity nes 109; Conserv
341 GAGTACACCCTGGAGGAAGCCCTGGCCGCCCTG
                                268 GTGAAGGCCCTGAAGGCCCTGCTGGGGGCCCCTG 300
                                                                                                                                                                                                                                   148 CCCCTCGGCACCCTCAACCCGCTGAAGCTCCTGCTGAGCAGCCTGGGGCATCCCCGTGAAC
                                                                                                                                                                                                  221 TACCGGCTGCCCGCCGAGCCGCTGGAGCAGCCTGAACCACCTAGGCCGCCAGGCCGGC
                                                                                                                                                                                                                                                                                                       161 GTCCTGGTTTCCGCCGGCAGCGCCTGCGCCCGAGATCCGCACCGATACCCGCCAGTAC
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Pred. No. 0.22;
0; Mismatches 104;
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APPLICANT: MARC J. Rubenfield et al.
TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PSEUDOMONAS;
TITLE OF INVENTION: AERUGINOSA FOR DIAGNOSTICS AND THERAPEUTICS
FILE REFERENCE: 107196.136
CURRENT APPLICATION UNMEER: US/09/252,991A
CURRENT FILING DATE: 1999-02-18
PRIOR APPLICATION NUMBER: US 60/074,788
PRIOR APPLICATION NUMBER: US 60/074,190
PRIOR TILING DATE: 1998-07-27
NUMBER: US 60/094,190
PRIOR FILING DATE: 1998-07-27
NUMBER: US 60/094,190
PRIOR FILING DATE: 1998-07-27
NUMBER: US 60/094,190
PRIOR FILING DATE: 1998-07-27
NUMBER: DS SEQ ID NOS: 33142
SEQ ID NO 13281
LENGTH: 432
US-09-252-991A-13281 RESULT 8
US-09-252-991A-13281/c
J. Sequence 13281, Application US/09252991A
J. Patent No. 6551795
J. GENERAL INFORMATION
J. APPLICANT: Marc J. Rubenfield et al.

14.8%;

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Score 46.2; I Pred. No. 0.27 0; Mismatches

DB 4;

Length 432;

158;

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RESULT 10
US-09-252-991A-12677
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US-09-252-991A-12820
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Sequence 12677, Application US/09252991A

Patent No. 6551795

GENERAL INFORMATION:
APPLICANT: MATCO J. Rubenfield et al.
APPLICANT: MATCO J. RUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TITLE OF INVENTION: AERUGINOSA FOR DIAGNOSTICS AND THERAPEUTICS

FILE REFERENCE: 107196;136

CURRENT APPLICATION NUMBER: US/09/252,991A
CURRENT APPLICATION NUMBER: US/09/252,991A
CURRENT FILING DATE: 1999-02-18

PRIOR APPLICATION NUMBER: US/09/252,991A
PRIOR APPLICATION NUMBER: US/09/252,991A
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TITLE OF INVENTION: AUCLEIC ACID AND AMINO ACID SEQUENCES RELATING
TITLE OF INVENTION: AUCLEIC ACID AND AMINO ACID SEQUENCES RELATING
TITLE OF INVENTION: AUCLEIC ACID AND AMINO ACID SEQUENCES RELATING
TITLE OF INVENTION: AUCLEIC ACID AND THERAPEUTICS
FILE REFERENCE: 107196,136
CURRENT FILING DATE: 1999-02-18
PRIOR APPLICATION NUMBER: US 60/074,788
PRIOR APPLICATION NUMBER: US 60/074,788
PRIOR APPLICATION NUMBER: US 60/094,190
PRIOR FILING DATE: 1998-07-27
NUMBER OF SEQ ID NOS: 33142
SEQ ID NO 12820
LENGTH: 1425
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Sequence 12820, Application US/09252991A patent No. 6531795
GENERAL INFORMATION:
APPLICANT: Marc J. Rubenfield et al.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ORGANISM: Pseudomonas
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               -252-991A-12820
                                                                                                                                                                                                                                                                                                            954 GCTGCCGGCCAACGAGCCGGGCAGCTCGATCATGCCCGGCAAGGTCAACCCGACCAGT
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                                                                                                                                                                                                                                                                                                                                                                                                                               CCTGGGCATCCCCGTGAACCACCTCATAGAGGGCTCCCAGAAGTGTGTGGCTGAGCTGGG 248
                                                                                                                                                                                                                                                                                                                                                                                                                                                                         CCACGAGCCGCTGGTCATCCTCCCGGCGCCCTGAAGAGCCTGGCGGTGGCCCTGATGAA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              GGCCGGGACCCTGGCCAACCCCCTCGGCACCCCTCAACCCCGCTGAAGCTCCTGCTGAGCAG
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Pred No. 0.27;
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US-09-252-991A-13122/c
US-09-252-991A-13122/c
Sequence 13122, Application US/09252991A
Patent No. 6551795
Patent No. 6551795
GENERAL INFORMATION:
APPLICANT: MATC J. Rubenfield et al.
APPLICANT: MATC J. Rubenfield et al.
APPLICANT: MATC J. RUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO P
TITLE OF INVENTION: AERUGINOSA FOR DIAGNOSTICS AND THERAPEUTICS
FILE REFERENCE: 107196.136
CURRENT APPLICATION NUMBER: US/09/252,991A
CURRENT FILING DATE: 1999-02-18
PRIOR APPLICATION NUMBER: US 60/074,788
PRIOR APPLICATION NUMBER: US 60/074,788
PRIOR APPLICATION NUMBER: US 60/094,190
PRIOR FILING DATE: 1998-07-27
NUMBER OF SEQ ID NOS: 33142
ENOTH: 1611
TYPE: DAM
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                                                                                                                                                                                                                                                                                                                                                                    ; ORGANISM: Pseudomonas aeruginosa US-09-252-991A-13122
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               PRIOR APPLICATION NUMBER: US 60/094,190
PRIOR FILING DATE: 1998-07-27
NUMBER OF SEQ ID NOS: 33142
SEQ ID NO 12677
LENGTH: 1428
                                                                                                                                                                                                                                                                                         Matches
                                                                                                                                                                                                                                                                                                                               Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Best Local Similarity Matches 141; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Query Match
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            661 CGCGGTGGGCACCGGGCTCAACGCGCCGAAGGGCCTTCGCCGACGCCATCGCCGCGGAAAT
                                                                                                                                                                                                                                                                                       al Similarity 47.
                                                                                                                                                                 69
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  9 CGCCGCCCTCCTGGGGCTCTGCGTGCCTGTCCTGCAGCTCCGCTCGTTCTTAGT
                                                                                                                                                                 GGGCTCGGCCAAGCCTGTGGCCCAGCCTGTCGCTGCGCTGGAGTCGGCGGCGGAGGCCGG
                                                                                                                                                                                                         CGCGGTTGGGCACCGGGCTCAACGCGCCGAAGGGCTTCGCCGACGCCATCGCCGCGGAAAT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TCCCCAGGCCGTGGGGGCCCTGAAGGCCCTGCTGGGGGGCCCTGACAGTGT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         CCTGGGCATCCCCGTGAACCACCTCATAGAGGGCTCCCAGAAGTGTGTGGGCTGAGCTGGG 248
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               CCACGAGCCGCTGGTCATCCTCTCCGGCGCCCTGAAGAGCCTTGGCGGTGGCCCTGATGAA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    GGCCGGGACCCTGGCCACCCTCGACCCTCAACCCGCTGAAGCTCCTGCTGAGCAG 188
       CCTGGGCATCCCCGTGAACCACCTCATAGAGGGCTCCCAGAAGTGTGTGGCTGAGCTGGG
                                                                                    GGCCGGGACCCTGGCCAACCCCCTCGGCACCCTCAACCCGCTGAAGCTCCTGCTGAGCAG
                                                                                                                            CGCCGCCGAATCGGGCCTGCCCTTCGTCGCCGCGCCCGAACAAGTTCGCCGCCCTGGCCGG
                                                                                                                                                                                                                                          caccaccercaracacceracacceracacacceracacceracacceracerracerracer
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  GATCGCCAACGACCTGCGCCTGCTCGGTTCCGGCCCACGCCCGGCCTTCGCCGAGGTGAA
                                            CCACGAGCCGCTGGTCATCCTCCGGCGCCCCTGAAGAGCCTGGCCGGTGGCCCTGATGAA
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                                                                                                                                                                                                                                                                                                         14.8%;
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                                                                                                                                                                                                                                                                                       Score 46.2; DB Pred. No. 0.27; O; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Score 46.2; DB 4;
Pred. No. 0.27;
D; Mismatches 158;
                                                                                                                                                                                                                                                                                                                          DB 4;
                                                                                                                                                                                                                                                                                                                            Length 1611;
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840

128 720

780

188

869

128

758

Gaps

287

110 265 170

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RESULT 13
US-09-252-991A-7185/c
; Sequence 7185, Application US/09252991A
; Sequence 7185, Application US/09252991A
; Patent No. 6551795
; Patent No. 6551795
; Patent No. 6551795
; APPLICANT: Marc J. Rubenfield et al.
TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PSEU
; TITLE OF INVENTION: AERUGINOSA FOR DIAGNOSTICS AND THERAPEUTICS
; FILE REFERENCE: 107196.136
; CURRENT APPLICATION NUMBER: US/09/252,991A
; CURRENT FILING DATE: 1999-02-18
; PRIOR APPLICATION NUMBER: US 60/074,788
; PRIOR APPLICATION NUMBER: US 60/094,190
; PRIOR FILING DATE: 1998-07-27
; NUMBER OF SEQ ID NO.7185
; SEQ ID NO.7185
; LENGTH: 1083
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         APPLICANT: MATC J: Rubenfield et al.
TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PSEUDOMONAS
TITLE OF INVENTION: ARROGINOSA FOR DIAGNOSTICS AND THERAPEUTICS
FILE REFERENCE: 107196.136
CURRENT PAPLICATION UNMEER: US/09/252,991A
CURRENT FILING DATE: 1999-02-18
PRIOR APPLICATION NUMBER: US 60/074,788
PRIOR APPLICATION NUMBER: US 60/074,788
PRIOR TILING DATE: 1998-07-18
PRIOR APPLICATION NUMBER: US 60/094,190
PRIOR TILING DATE: 1998-07-27
SEQ ID NO 7316
LENGTH: 729
LENGTH: 729
TYPE: DNA
ORGANIUM: PSEUdomonas aeruginosa
US-09-252-991A-7316
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US-09-252-991A-7316
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GENERAL INFORMATION:
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Best Local
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          86 TGGCCCAGCCTGTCGCTGCGCTGGAGTCGGCGGGGCCGGGGCCGGGACCCTGGCCA 145
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Pred. No. 0.67;
0; Mismatches 123;
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; ORGANISM: Pseudomonas aeruginosa
US-09-252-991A-7304
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   RESULT 14
US-09-252-991A-7304/c
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; ORGANISM: Pseudomonas aeruginosa
US-09-252-991A-7185
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              GENERAL INFORMATION:
APPLICANT: Marc J: Rubenfield et al.
APPLICANT: Marc J: Rubenfield et al.
APPLICANT: Marc J: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PSEUDOMONAS
TITLE OF INVENTION: AERUGINOSA FOR DIAGNOSTICS AND THERAPEUTICS
FILE REFERENCE: 107196.136
CURRENT APPLICATION NUMBER: US/09/252,991A
CURRENT FILING DATE: 1999-02-18
PRIOR APPLICATION NUMBER: US 60/074,788
PRIOR APPLICATION NUMBER: US 60/074,188
PRIOR FILING DATE: 1998-02-18
PRIOR APPLICATION NUMBER: US 60/094,190
                                                                                                                                                                                                                                                                                                                                                                                                                 Query Match
Best Local S
Matches 131
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   286 GGGCGCTGGCGCGCGCGCACCCAACAGTCCACGGCCGAGATCGAGACCCCTGATCGGTGCCT 227
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                                                                                                                                                                                                                                                                   86 TGGCCCAGCCTGTCGCTGGCGTGGAGTCGGCGGGAGGCCGGGGCCGGGGACCCTGGCCA 145
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                                                                                                                                                                                                                                          GGGCGCTGGCGCGCGCACCCAACAGTCCACGGCCGAGATCGAGACCCTGATCGGTGCCT
                                                                                             ACCAGAGCGTCGACGACGCGTTGCAGACCGAGGCGGCGCTGGGCAACATCGCCACGGCGG
                                                                                                                                                    TGCAGAATGGCACGCAGCAGCGGTGCAGCGTATGCAGCGCAGCCACCAGTTG---GTGG
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                                                                                                                                                                                                                                                                                                                                                                                                            14.2%; Score 44.2; DB 4;
51.0%; Pred. No. 0.66;
tive 0; Mismatches 123;
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265

237

177

Mon Sep

В

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TGGCGCTGATCCAGCAG

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US-08-555-669-11
Sequence 11, Application US/08555669
Sequence 17, Application US/08555669
Sequence 17, Application US/08555669
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC Compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/555,669
FILING DATE: 13-NOV-1995
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: Halluin, Albert P.
REGISTRATION NUMBER: 25,227
REFERENCE/DOCKET NUMBER: 8389-030
TELECOMMUNICATION INFORMATION:
TELEPAN: 415-854-3660
TELEFAN: 415-854-3660
TELEFAN: 415-854-3660
TELEFAN: 66141 PENNIE
INFORMATION FOR SEQ ID NO: 11:
SEQUENCE CHARROTERISTICS:
LENGTH: 2543 base pairs
TYPE: nucleic acid
STRANDEDNESS: unknown
MOLECULE TYPE: CDNA
REARCY CDS
                                                                                                                                     DЬ
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                                                                                                                                                                                                                                                                                                                                                                                                                                       ; NAME/KEY:
; LOCATION:
US-08-555-669-11
                                                             В
                                                                                                   γQ
                                                                                                                                                                                                                                                                                                                                                             Query Match 14.2%; Score 44.2; DB 1; Length 2543; Best Local Similarity 47.3%; Pred. No. 0.66; Matches 133; Conservative 0; Mismatches 148; Indels 0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       APPLICANT: Brewton, Richard G.
APPLICANT: Mayne, Richard
TITLE OF INVENTION: TYPE IX COLLAGEN AND FRAGMENTS THEREOF
NUMBER OF SEQUENCES: |32
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ADDRESSEE: Pennie & STREET: 1155 Avenue CITY: New York STATE: New York
  1451
                                                                        1391
                                                                                                                                           1331 CGGGGTCCGGGAGGTGCCGAAGGCCCTAAGGGAGACCAGGGTATTGCAGGTTCCGACGGT 1390
                                                                                                                                                                                                                                                                                       1271 GGCAGCATGGGAGACCCCGGCCTTCCAGGCCCCCAGGGCCTCCGAGGTGACGTGGGCGAC
186 CAGCCTGGGCATCCCCGTGAACCACCTCATAGAGGGCTCCCAGAAGTGTGTGGCTGAGCT 245
                                                                                                                                                                                  126 CGGGGCCGGGACCCTGGCCAACCCCCTCGGCACCCTCAACCCGCTGAAGCTCCTGCTGAG 185
                                                                                                                                                                                                                                                     66 AGTGGGCTCGGCCAAGCCTGTGGCCCAGCCTGTCGCTGGAGTCGGCGGGGGGAGGC 125
                                                                     USA
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of the Americas
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Search completed: September 20, 2003, 01:40:46 Job time: 37.0684 secs

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Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries
                                                                                                                                                                                                                                         Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.
                                                                                                                                                                                    Score
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seq length: 2000000000
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               of hits satisfying chosen parameters:
                                                                                                                                                                                                                                                                                  published_Applications_NA:*

1: /cgn2_6/ptcodata/1/pubpna/US07_PUBCOMB.seq:*

2: /cgn2_6/ptcodata/1/pubpna/US06_NEW_PUB.seq:*

3: /cgn2_6/ptcodata/1/pubpna/US06_NEW_PUB.seq:*

4: /cgn2_6/ptcodata/1/pubpna/US06_NEW_PUB.seq:*

5: /cgn2_6/ptcodata/1/pubpna/US07_NEW_PUB.seq:*

6: /cgn2_6/ptcodata/1/pubpna/US08_NEW_PUB.seq:*

7: /cgn2_6/ptcodata/1/pubpna/US08_PUBCOMB.seq:*

8: /cgn2_6/ptcodata/1/pubpna/US08_PUBCOMB.seq:*

10: /cgn2_6/ptcodata/1/pubpna/US08_PUBCOMB.seq:*

11: /cgn2_6/ptcodata/1/pubpna/US09_PUBCOMB.seq:*

12: /cgn2_6/ptcodata/1/pubpna/US09_PUBCOMB.seq:*

13: /cgn2_6/ptcodata/1/pubpna/US09_NEW_PUB.seq:*

14: /cgn2_6/ptcodata/1/pubpna/US10B_PUBCOMB.seq:*

15: /cgn2_6/ptcodata/1/pubpna/US10B_PUBCOMB.seq:*

16: /cgn2_6/ptcodata/1/pubpna/US10B_PUBCOMB.seq:*

16: /cgn2_6/ptcodata/1/pubpna/US10B_PUBCOMB.seq:*

17: /cgn2_6/ptcodata/1/pubpna/US10B_PUBCOMB.seq:*

17: /cgn2_6/ptcodata/1/pubpna/US10B_PUBCOMB.seq:*
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312
1 atgaagctcgccgccctcct.....gggccctgacagtgtttggc 312
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Match
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3 US-10-081-817-3

4 US-10-237-435-6

2 US-10-210-951-27

2 US-09-989-722-407

1 US-09-989-727-407

1 US-09-989-727-407

1 US-09-989-727-407

1 US-09-989-727-407

2 US-09-991-073-407

2 US-09-991-073-407

2 US-09-991-073-407

2 US-09-991-073-407

2 US-09-991-08-407-407

3 US-09-991-08-407-407

4 US-09-993-604-407

5 US-09-993-721-407

6 US-09-993-721-407

7 US-09-993-721-407
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          [4 ; Search time 124.366 Seconds
(without alignments)
6171.248 Million cell updates/sec
 Sequence 3, Appli
Sequence 6, Appli
Sequence 27, Appl
Sequence 407, App
                                                                                                                                                                                  Description
                                                                                                                                                                  US-10-061-61/-3
Sequence 3, Application US/10081817
Publication No. US20020183501A1
GENERAL INFORMATION:
APPLICANT: Polyak, Kornelia
APPLICANT: Porter, Dale
APPLICANT: Porter, Dale
APPLICANT: RYOP, Ian
TITLE OF INVENTION: HIN-1, A TUMOR SUPPRESSOR GENE
FILE REFERENCE: 00530-094001
CURRENT APPLICATION NUMBER: US/10/081,817
CURRENT FILING DATE: 2002-05-31
PRIOR APPLICATION NUMBER: 60/270,973
PRIOR APPLICATION NUMBER: 60/270,973
PRIOR APPLICATION NUMBER: 60/351,908
PRIOR FILING DATE: 2001-02-23
PRIOR APPLICATION NUMBER: 60/351,908
PRIOR FILING DATE: 2002-01-25
NUMBER OF SEQ ID NOS: 32
SEQ ID NO 3
SEQ ID NO 3
SEQ ID NO 3
CRGANISM: Homo sapiens
US-10-081-817-3
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                     Ω
                                        Вþ
                                                                                                                               Query Match
Best Local Similarity
Matches 312; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    121 GAGGCCGGGGCCGGGACCCTGGCCAACCCCTCAACCCGCTGAAGCTCCTG
                                          100.0%; Score 312; DB 13; ilarity 100.0%; Pred. No. 2e-64; Conservative 0; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            US-09-989-293A-407
US-09-989-735-407
US-09-990-444-407
US-09-991-181-407
US-09-991-89-730-407
US-09-990-653-407
US-09-993-653-407
US-09-997-653-407
US-09-997-666-407
US-09-997-666-407
US-09-997-666-407
US-09-997-668-407
US-09-990-438-407
US-09-990-438-407
US-09-990-438-407
US-09-991-157-407
US-09-991-157-407
US-09-997-514-407
US-09-997-514-407
US-09-997-514-407
US-09-997-518-407
US-09-997-518-407
US-09-997-658-407
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                                                                                                                                                         Length 312;
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Result No.

0;

Gaps

120 60 60 Minimum DB Maximum DB

Scoring table: Title: Perfect score: Sequence:

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RESULT 2

US-10-237-435-6

Sequence 6, Application US/10237435

PUBLICATION NO. US20030124580A1

GENERAL INFORMATION:
APPLICANT: WALKEY, MICHAel G.
APPLICANT: WALKEY, LYND E.
APPLICANT: WALKEY, LYND E.
TITLE OF INVENTION: LUNG SURFACTANT MOLECULES
FILE REFERENCE: PB-0019 US
CURRENT APPLICATION NUMBER: US/10/237,435
CURRENT FILING DATE: 00-00-006
PRIOR APPLICATION NUMBER: 60/317,822
PRIOR APPLICATION NUMBER: 60/317,822
PRIOR FILING DATE: 09-07-2001
NUMBER OF SEQ ID NOS: 9
SOFTMARE: PERL PROGRAMIAM: HOMO Sapiens
FEATURE: DNA
ORGANIAM: HOMO Sapiens
FEATURE: HOMO Sapiens
          RESULT 3
US-10-210-951-27
Sequence 27, Application US/10210951
Publication No. US20030170228A1
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al Similarity |99.4%;
310; Conservative
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                                                                                                                                                                                                           CTGAGCAGCCTGGGCATCCCCGTGAACCACCTCATAGAGGGCTCCCAGAAGTGTGTGGCT
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                                                                                                    428
                                                                                                                                  312
                                                                                                                                                                                                                                                                                                                                                                                                                                               Score 308.8; DB 14; Length Pred. No. 1e-63; O; Mismatches 2; Indels
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APPLICANT: WOOD, William I.

TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE TREATMENT OF TUMOR FILE REFERENCE: P293IR101

CURRENT APPLICATION NUMBER: US/10/210,951

CURRENT FILING DATE: 2002-08-02

PRIOR APPLICATION NUMBER: 60/014699

PRIOR FILING DATE: 1996-04-01

PRIOR FILING DATE: 1996-09-23

PRIOR APPLICATION NUMBER: 60/059121

PRIOR APPLICATION NUMBER: 60/059121

PRIOR APPLICATION NUMBER: 60/059352

PRIOR FILING DATE: 1997-07-17

PRIOR APPLICATION NUMBER: 60/062037

PRIOR FILING DATE: 1997-10-17

PRIOR FILING DATE: 1997-10-17

PRIOR APPLICATION NUMBER: 60/063045

PRIOR APPLICATION NUMBER: 60/063045

PRIOR APPLICATION NUMBER: 60/063046

PRIOR FILING DATE: 1997-10-24

PRIOR FILING DATE: 1997-10-24

PRIOR FILING DATE: 1997-11-24

PRIOR FILING DATE: 1997-11-24
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NUMBER OF SEQ ID NOS: 258
SEQ ID NO 27
LENGTH: 569
TYPE: DNA
ORGANIZM: Homo sapiens
US-10-210-951-27
                                                                                                                                                                                                                                                                                                                                                      Matches
                                                                                                                                                                                                                                                                                                                                                                  Query Match
Best Local
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        APPLICANT:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          APPLICANT: Ashkenazi, Avi J.
APPLICANT: Goddard, Audrey
APPLICANT: Godowski, Paul J
301 ACAGTGTTTGGC 312
|||||||||||
379 ACAGTGTTTGGC 390
                                                                                                          al Similarity
310; Conserv
                                                 Pan, James
Pitti, Robert M.
Roy, Margaret Ann
Smith, Victoria
Stone, Donna M.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Goddard, Audrey
Godowski, Paul J.
Gurney, Austin L.
Hillan, Kenneth J.
Marsters, Scot A.
                                                                                                                                                                                                                                                                                                                                                 Conservative
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RESULTA 10

RESULTA 10

REPLICANT: ASPECTANTON

REPLICANT: Baker, Eval p.
APPLICANT: Boods, Ministin J.
APPLICANT: Boods, Ministin J.
APPLICANT: Boods, Ministin J.
APPLICANT: Boods, Milliam I.
APPLICANT: Watlands, Colin K.
APPLI
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PRIOR FILING DATE: 1998-06-04
PRIOR PELICATION NUMBER: 60/088030
PRIOR PELICATION NUMBER: 60/088033
PRIOR FILING DATE: 1998-06-04
PRIOR APPLICATION NUMBER: 60/08326
PRIOR PRIOR PELICATION NUMBER: 60/08326
PRIOR PRIOR PELICATION NUMBER: 60/088167
PRIOR APPLICATION NUMBER: 60/088167
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PRIOR PELICATION NUMBER: 60/088202
PRIOR PELICATION NUMBER: 60/088217
PRIOR PELICATION NUMBER: 60/088217
PRIOR PELICATION NUMBER: 60/088217
PRIOR PELICATION NUMBER: 60/088734
PRIOR PELICATION NUMBER: 60/088734
PRIOR PELICATION NUMBER: 60/088734
PRIOR PELICATION NUMBER: 60/088742
PRIOR PELICATION NUMBER: 60/088742
PRIOR PELICATION NUMBER: 60/088742
PRIOR PELICATION NUMBER: 60/088742
PRIOR PELICATION NUMBER: 60/088810
PRIOR PELICATION NUMBER: 60/088810
PRIOR PELICATION NUMBER: 60/088826
PRIOR PELICATION NUMBER: 60/088944
PRIOR PELICATION NUMBER: 60/089512
PRIOR APPLICATION NUMBER: 60/089512
PRIOR APPLICATION NUMBER: 60/089512
PRIOR APPLICATION NUMBER: 60/08959
PRIOR APPLICATION NUMBER: 60/08959
PRIOR APPLICATION NUMBER: 60/08959
PRIOR PELICATION NUMBER: 60/08994
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PRIOR APPLICATION NUMBER: 60/09035
PRIOR APPLICATION NUMBER: 60/090429
PRIOR APPLICATION NUMBER: 60/090429
PRIOR APPLICATION NUMBER: 60/090431
PRIOR APPLICATION NUMBER: 60/090431
PRIOR FILING DATE: 1998-06-24
PRIOR FILING DATE: 1998-06-24
PRIOR APPLICATION NUMBER: 60/090444
PRIOR APPLICATION NUMBER: 60/090445
PRIOR APPLICATION NUMBER: 60/090445
PRIOR APPLICATION NUMBER: 60/090472
PRIOR APPLICATION NUMBER: 60/09053
PRIOR FILING DATE: 1998-06-24
PRIOR APPLICATION NUMBER: 60/09053
PRIOR APPLICATION NUMBER: 60/090540
PRIOR APPLICATION NUMBER: 60/090540
PRIOR APPLICATION NUMBER: 60/090540
PRIOR APPLICATION NUMBER: 60/090542
PRIOR APPLICATION NUMBER: 60/09057
PRIOR APPLICATION NUMBER: 60/09057
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PRIOR APPLICATION NUMBER: 60/09057
PRIOR PILING DATE: 1998-06-24
PRIOR APPLICATION NUMBER: 60/09057
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Best Local S
Matches 310
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OR APPLICATION NUMBER: 60/090694
OR APPLICATION NUMBER: 60/090695
OR FILING DATE: 1998-06-25
OR FILING DATE: 1998-06-26
OR PPLICATION NUMBER: 60/090863
OR FILING DATE: 1998-06-26
OR APPLICATION NUMBER: 60/091360
OR FILING DATE: 1998-06-26
OR FILING DATE: 1998-07-01
OR APPLICATION NUMBER: 60/09154
OR FILING DATE: 1998-07-02
OR FILING DATE: 1998-07-02
OR APPLICATION NUMBER: 60/091519
OR APPLICATION NUMBER: 60/091519
OR FILING DATE: 1998-07-02
OR APPLICATION NUMBER: 60/091626
OR FILING DATE: 1998-07-02
OR APPLICATION NUMBER: 60/09163
OR APPLICATION NUMBER: 60/091978
OR APPLICATION NUMBER: 60/092182
OR FILING DATE: 1998-07-07
OR APPLICATION NUMBER: 60/092182
OR FILING DATE: 1998-07-07
OR APPLICATION NUMBER: 60/092182
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310; Conserv
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ilarity |99.4%;
Conservative
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Pred. No. 1e-63;
0; Mismatches 2;
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APPLICANT: Tumas, Daniel
APPLICANT: Williams, P. Mickey
APPLICANT: Williams, P. Mickey
APPLICANT: Williams, P. Mickey
APPLICANT: Zhang, Zemin
ITTLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
ITTLE OF INVENTION: Acids Encoding the Same
FILE REFERENCE: P2730PlC62
CURRENT APPLICATION NUMBER: 60/049787
PRIOR APPLICATION NUMBER: 60/049787
PRIOR APPLICATION NUMBER: 60/049787
PRIOR APPLICATION NUMBER: 60/062250
PRIOR APPLICATION NUMBER: 60/062250
PRIOR APPLICATION NUMBER: 60/065186
PRIOR APPLICATION NUMBER: 60/065311
PRIOR APPLICATION NUMBER: 60/065311
PRIOR APPLICATION NUMBER: 60/065311
PRIOR APPLICATION NUMBER: 60/065311
PRIOR APPLICATION NUMBER: 60/066770
PRIOR APPLICATION NUMBER: 60/075945
PRIOR APPLICATION NUMBER: 60/075945
PRIOR APPLICATION NUMBER: 60/078910
PRIOR APPLICATION NUMBER: 60/083322
PRIOR APPLICATION NUMBER: 60/084600
PRIOR APPLICATION NUMBER: 60/084600
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APPLICANT: Baker, Kevin P.
APPLICANT: Botstein, David
APPLICANT: Botstein, David
APPLICANT: Eaton, Dan L.
APPLICANT: Ferrara, Napoleone
APPLICANT: Ferrara, Napoleone
APPLICANT: Gerritsen, Mary E.
APPLICANT: Gerritsen, Mary E.
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Paoni, Nicholas F.
Roy, Margaret Ann
Stewart, Timothy A.
Tumas, Daniel
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Kljavin, Ivar J.
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Query Match

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89, 27	APPLICANT: Goddward, Audrey APPLICANT: Goddward, Paull J. APPLICANT: Grimaldil, Christopher APPLICANT: Grimaldil, Christopher APPLICANT: Grimaldil, Christopher APPLICANT: Grimaldil, Tohristopher APPLICANT: Grimaldil, Tohristopher APPLICANT: Nagier, Mary A. APPLICANT: Paoni, Nicholas F. APPLICANT: Roy, Margaret Ann APPLICANT: Roy, Margaret Ann APPLICANT: Stewart, Timothy A. APPLICANT: Grimas, Daniel APPLICANT: Watanabe, Colin K. APPLICANT: Williams, P. Mickey APPLICANT: Wood, Williams I. APPLICANT: Stang, Zemin TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic TITLE OF INVENTION: Acids Encoding the Same	ACACTGTTTGGC 312 ACACTGTTTGGC 390 ACACTGTTGGC 390 ACACTGTTTGGC 390 ACACTGTTTGGC 390 ACACTGTTTGGC 390 A	Pest Local Similarity 99.4%; Pred. No. 1e-63; Matches 310; Conservațive 0; Mismatches 2; Indels 0; Gaps 0; 1 ATGAAGCTCGCCGCCCTCCTGGGGCTCTGCGTGGCCCTGCTGCAGCTCCGGCTGCTGCT 60 1
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PRIOR PPLICATION NUMBER: 60/091633
PRIOR PPLICATION NUMBER: 60/091978
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PRIOR APPLICATION NUMBER: 60/092182
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APPLICANT:
APPLICANT:
APPLICANT:
               APPLICANT: Zhang, Zemin
TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
TITLE OF INVENTION: Acids Encoding the Same
FILE REFERENCE: P2730P1C65
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T: Baker, Kevin P.
T: Baker, Kevin P.
T: Botstein, David
T: Desnoyers, Luc
T: Eaton, Dan L.
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T: Gerber, Hanspeter
T: Gerritsen, Mary E.
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Roy, Margaret Ann
Stewart, Timothy A.
Tumas, Daniel
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Williams, P. Mickey
Wood, William I.
Zhang, Zemin
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CURRENT APPLICATION NUMBER: US/09/989,727

CURRENT FILING DATE: 1207-01-11-19

PRIOR FILING DATE: 1997-06-16

PRIOR FILING DATE: 1997-07-17

PRIOR FILING DATE: 1997-11-12

PRIOR APPLICATION UNMEER: 60/065311

PRIOR APPLICATION UNMEER: 60/075945

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PRIOR FILING DATE: 1998-05-07

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PRIOR APPLICATION UNMEER: 60/087607

PRIOR APPLICATION UNMEER: 60/087807

PRIOR APPLICATION UNMEER: 60/088025

PRIOR APPLICATION UNMEER: 60/088026

PRIOR PILING DATE: 1998-06-04

PRIOR APPLICATION UNMEER: 60/088026

PRIOR PILING DATE: 1998-06-04

PRIOR APPLICATION UNMEER: 60/088026

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Sequence 407, Application US/09989731
Patent NO. US20020103125A1
GENERAL INFORMATION:
APPLICANT: Ashkenazi, Avi J.
APPLICANT: Baker, Kevin P.
APPLICANT: Betset, David
APPLICANT: Desnoyers, Luc
APPLICANT: Desnoyers, Luc
APPLICANT: Eston, Dan L.
APPLICANT: Ferrara, Napoleone
APPLICANT: Ferrara, Napoleone
APPLICANT: Gerrher, Hanspeter
APPLICANT: Gerrher, Hanspeter
APPLICANT: Goddard, Audrey
APPLICANT: Goddard, Audrey
APPLICANT: Grimaldi, J. Christopher
APPLICANT: Grimaldi, J. Christopher
APPLICANT: Kljavin, Ivar J.
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PRIOR FILING DATE: 1998-06-25
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PRIOR PRIOR APPLICATION NUMBER: 60/091478
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PRIOR APPLICATION NUMBER: 60/091633
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APPLICANE: WOOL, William 1.

APPLICANE: WOOL, William 1.

PITTE OF INVENTION. Schedes Encoding the Same Polypeptides and Nucleic TITTLE OF INVENTION. Schedes Encoding the Same Fill Represence: p201201270

CURRENT FILLING DATE: 1907-10-120

PRIOR APPLICATION NUMBER: 05/05/89,731

CURRENT FILLING DATE: 1997-10-120

PRIOR APPLICATION NUMBER: 05/05/811

PRIOR APPLICATION NUMBER: 05/065311

PRIOR APPLICATION NUMBER: 05/078910

PRIOR APPLICATION NUMBER: 05/078927

PRIOR APPLICATION NUMBER: 05/
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Stewart, Timothy A.
Tumas, Daniel
Watanabe, Colin K.
Williams, P. Mickey
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Pan, James
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Query Match Best Local S Matches 310

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RESULT 8 US-09-989-731-407 "Caquence 407, AF "RE20/

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RESULT 9
US-09-989-732-407
; Sequence 407, Application US/09989732
; Patent No. US20020133463A1
; GENERAL INFORMATION:
; APPLICANT: Ashkenazi, Avi J.
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OR APPLICATION NUMBER: 60/99057
OR ETILING DATE: 1998-06-24
OR FILING DATE: 1998-06-25
OR APPLICATION NUMBER: 60/990676
OR FILING DATE: 1998-06-25
OR APPLICATION NUMBER: 60/990690
OR FILING DATE: 1998-06-25
OR APPLICATION NUMBER: 60/990694
OR FILING DATE: 1998-06-25
OR APPLICATION NUMBER: 60/990695
OR FILING DATE: 1998-06-25
OR APPLICATION NUMBER: 60/990696
OR FILING DATE: 1998-06-26
OR APPLICATION NUMBER: 60/990863
OR FILING DATE: 1998-06-26
OR FILING DATE: 1998-06-26
OR FILING DATE: 1998-06-26
OR APPLICATION NUMBER: 60/991360
OR FILING DATE: 1998-07-01
OR APPLICATION NUMBER: 60/09154
OR FILING DATE: 1998-07-02
OR APPLICATION NUMBER: 60/09159
OR FILING DATE: 1998-07-02
OR APPLICATION NUMBER: 60/091626
OR FILING DATE: 1998-07-02
OR APPLICATION NUMBER: 60/09163
OR APPLICATION NUMBER: 60/09163
OR APPLICATION NUMBER: 60/09163
OR APPLICATION NUMBER: 60/09167
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310; Conservative
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Pred. No. 1e-63;
0; Mismatches 2;
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OR APPLICATION NUMBER: 60/088742
OR FILING DATE: 1998-06-10
OR APPLICATION NUMBER: 60/088810
OR APPLICATION NUMBER: 60/088826
OR FILING DATE: 1998-06-10
OR APPLICATION NUMBER: 60/088826
OR FILING DATE: 1998-06-11
OR APPLICATION NUMBER: 60/088861
OR APPLICATION NUMBER: 60/089861
OR APPLICATION NUMBER: 60/089861
OR APPLICATION NUMBER: 60/089810
OR APPLICATION NUMBER: 60/089510
OR APPLICATION NUMBER: 60/089512
OR FILING DATE: 1998-06-16
OR APPLICATION NUMBER: 60/089514
OR APPLICATION NUMBER: 60/089516
OR APPLICATION NUMBER: 60/089517
OR APPLICATION NUMBER: 60/089518
OR APPLICATION NUMBER: 60/089519
OR APPLICATION NUMBER: 60/090252
OR APPLICATION NUMBER: 60/090355
OR APPLICATION NUMBER: 6

FILING DATE: 1998-0 APPLICATION NUMBER:	PRIOR FILING DATE: 1997-11-13 PRIOR APPLICATION NUMBER: 60/076945 PRIOR APPLICATION NUMBER: 60/075945 PRIOR FILING DATE: 1998-03-25 PRIOR FILING DATE: 1998-03-25 PRIOR FILING DATE: 1998-03-20 PRIOR APPLICATION NUMBER: 60/078910 PRIOR APPLICATION NUMBER: 60/078910 PRIOR APPLICATION NUMBER: 60/083322 PRIOR APPLICATION NUMBER: 60/083322 PRIOR APPLICATION NUMBER: 60/084600 PRIOR FILING DATE: 1998-05-07 PRIOR APPLICATION NUMBER: 60/087106 PRIOR APPLICATION NUMBER: 60/087607 PRIOR APPLICATION NUMBER: 60/087607 PRIOR APPLICATION NUMBER: 60/087609 PRIOR APPLICATION NUMBER: 60/087827 PRIOR PILING DATE: 1998-06-02 PRIOR APPLICATION NUMBER: 60/088021	CANY: Stewa CANY: Guara Watan CANY: Watan CANY: Waltan CANY: Will CANY: Will CANY: Will CANY: CA	Baker, Kevin P. Botstein, David Desnoyers, Luc Eaton, Dan L. Ferrara, Napoleone Fong, Sherman Gerber, Hanspeter Gerritsen, Mary E. Goddard, Audrey Godowski, Paul J. Grimaldi, J. Christ Gurney, Austin L. Kljavin, Ivar J. Napier, Mary A. Pan, James Paoni, Nicholas F. Paoni, Margaret Ann
APPLICATION NETLING DATE:	APPLICATION FILING DATE:	PRIOR APPLICATION NUMBER: 60/08824 PRIOR ETLING DATE: 1998-06-10 PRIOR ETLING DATE: 1998-06-10 PRIOR ETLING DATE: 1998-06-10 PRIOR FILING DATE: 1998-06-10 PRIOR REPLICATION NUMBER: 60/08858 PRIOR FILING DATE: 1998-06-11 PRIOR APPLICATION NUMBER: 60/08861 PRIOR FILING DATE: 1998-06-11 PRIOR PRIOR ETLING DATE: 1998-06-12 PRIOR FILING DATE: 1998-06-12 PRIOR FILING DATE: 1998-06-16 PRIOR FILING DATE: 1998-06-16 PRIOR FILING DATE: 1998-06-16 PRIOR FILING DATE: 1998-06-16 PRIOR PRIOR APPLICATION NUMBER: 60/089512 PRIOR PRILING DATE: 1998-06-16 PRIOR PRILING DATE: 1998-06-16 PRIOR PRILING DATE: 1998-06-16 PRIOR FILING DATE: 1998-06-16	APPLINA STREET

APPLICATION NUMBER: FILING DATE: 1998-00 APPLICATION NUMBER: FILING DATE: 1998-00

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5-24
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Pred. No. 1e-63;
0; Mismatches 2;
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APPLICANT: "Humas, Danie!
APPLICANT: Williams, P. Mickey
APPLICANT: Williams, P. Mickey
APPLICANT: Williams, P. Mickey
APPLICANT: Wood, William I

APPLICANT: Wood, William I

TITLE OF INVENTION: Acids Encoding the Same
FILE OF INVENTION: Acids Encoding the Same
GURRENT FILING DATE: 2001-11-14

PRIOR APPLICATION NUMBER: US/09/991,073

CURRENT FILING DATE: 1997-06-16

PRIOR APPLICATION NUMBER: 60/062250

PRIOR APPLICATION NUMBER: 60/06516

PRIOR APPLICATION NUMBER: 60/065311

PRIOR APPLICATION NUMBER: 60/07845

PRIOR FILING DATE: 1997-11-12

PRIOR APPLICATION NUMBER: 60/07845

PRIOR FILING DATE: 1998-03-20

PRIOR APPLICATION NUMBER: 60/08322

PRIOR APPLICATION NUMBER: 60/08709

PRIOR APPLICATION NUMBER: 60/088021
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US-09-991-073-407
; Sequence 407, Application US/09991073
; Patent No. US20020127576A1
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APPLICANT
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APPLICANT: Baker, Kevin P.
APPLICANT: Botstein, David
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Stewart, Timothy A.
Tumas, Daniel
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Kljavin, Ivar
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Gerritsen, Mary E.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Fong, Sherman
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Eaton, Dan L.
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Query Match Best Local S Matches 310

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APPLICATION NUMBER: 60/088026

998-06-04

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PRIOR PRIOR PRIOR PRIOR

1998-06-04 1998-06-04 1998-06-04

60/088033

NR APPLICATION NUMBER: 60/08
R FILLING DATE: 1998-06-04
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PRIOR APPLICATION NUMBER: 60/090252
PRIOR APPLICATION NUMBER: 60/090254
PRIOR APPLICATION NUMBER: 60/090254
PRIOR APPLICATION NUMBER: 60/090349
PRIOR FILING DATE: 1998-06-23
PRIOR APPLICATION NUMBER: 60/090429
PRIOR APPLICATION NUMBER: 60/090439
PRIOR APPLICATION NUMBER: 60/090431
PRIOR FILING DATE: 1998-06-24
PRIOR PRIOR APPLICATION NUMBER: 60/090444
PRIOR PRILING DATE: 1998-06-24
PRIOR APPLICATION NUMBER: 60/090445
PRIOR APPLICATION NUMBER: 60/090444
PRIOR FILING DATE: 1998-06-24
PRIOR APPLICATION NUMBER: 60/090445
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PRIOR APPLICATION NUMBER: 60/090447
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PRIOR APPLICATION NUMBER: 60/090676
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PRIOR APPLICATION NUMBER: 60/090676
PRIOR APPLICATION NUMBER: 60/090695
PRIOR APPLICATION NUMBER: 60/090696
PRIOR PILING DATE: 1998-06-25
PRIOR APPLICATION NUMBER: 60/090696
PRIOR APPLICATION NUMBER: 60/090151
PRIOR APPLICATION NUMBER: 60/09151
PRIOR APPLICATION NUMBER: 60/091
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Best Local Similarity
Matches 310; Conserv
                                                                                                                                                                                                                                                                           FILING DATE: 1998-07-07
APPLICATION NUMBER: 60/091982
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APPLICATION NUMBER: 60/092182
FILING DATE: 1998-07-09
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   61 TTCTTAGTGGGCTCGGCCAAGCCTGTGGCCCAGCCTGTCGCTGCGCTGGAGTCGGCGGCG
                                                      ATGAAGCTCGCCGCCCTCCTGGGGCTCTGCGTGGCCCTGTCCTGCAGCTCCGCTCGTGCT
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Pred. No. 1e-63;
0; Mismatches 2;
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PRIOR FILING DATE: 1998-06-04
PRIOR APPLICATION NUMBER: 60/088167
PRIOR APPLICATION NUMBER: 60/088202
PRIOR APPLICATION NUMBER: 60/088202
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PRIOR APPLICATION NUMBER: 60/088212
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PRIOR APPLICATION NUMBER: 60/088826
PRIOR FILING DATE: 1998-06-10
PRIOR APPLICATION NUMBER: 60/088826
PRIOR PILING DATE: 1998-06-10
PRIOR APPLICATION NUMBER: 60/088826
PRIOR APPLICATION NUMBER: 60/089105
PRIOR APPLICATION NUMBER: 60/089512
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PRIOR APPLICATION NUMBER: 60/089599
PRIOR APPLICATION NUMBER: 60/089909
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PRIOR APPLICATION NUMBER: 60/06570 PRIOR RILING DATE: 1997-11-24 PRIOR RIPLICATION NUMBER: 60/075945 PRIOR APPLICATION NUMBER: 60/075945 PRIOR FILING DATE: 1998-02-25 PRIOR FILING DATE: 1998-03-20 PRIOR RPLICATION NUMBER: 60/08332 PRIOR RPLICATION NUMBER: 60/084600 PRIOR RPPLICATION NUMBER: 60/084600 PRIOR APPLICATION NUMBER: 60/084600 PRIOR APPLICATION NUMBER: 60/084600 PRIOR APPLICATION NUMBER: 60/087106	NAT EILING DATE: 2001-11-14 APPLICATION NUMBER: 60/049787 FILING DATE: 1997-06-16 APPLICATION NUMBER: 60/062250 FILING DATE: 1997-10-17 APPLICATION NUMBER: 60/065186 FILING DATE: 1997-11-12 APPLICATION NUMBER: 60/065311 FILING DATE: 1997-11-13	NT: Tumas, Da NT: Watanabe, NT: Williams, NT: Zhang, Ze TINVENTION: S FINVENTION: S FINVENTION: S FIRENCE: P2730 APPLICATION		SULT 11 -09-90-42-407 -09-90-90-42-407 -09-90-90-42-407 -09-90-90-42-407 -09-90-90-42-407 -09-90-90-42-407 -09-90-90-42-407 -09-90-90-42-407 -09-90-90-42-407 -09-90-90-42-407 -09-90-90-90-42-407 -09-90-90-90-42-407 -09-90-90-90-90-42-407 -09-90-90-90-90-42-407 -09-90-90-90-90-90-90-42-407 -09-90-90-90-90-90-90-90-90-90-90-90-90-	
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PRIOR PILLING DATE: 1998-06-25
PRIOR PILLING DATE: 1998-06-25
PRIOR PILLING DATE: 1998-06-25
PRIOR PILLING DATE: 1998-06-26
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APPLICANT: ASKRENZIA. AVI. A
APPLICANT: Bactacin, David
APPLICANT: Bestevin, David
APPLICANT: Bestop, David
APPLICANT: Bestop, David
APPLICANT: Eston, David
APPLICANT: Eston, David
APPLICANT: Everara, Napoleone
APPLICANT: Goristan, Mary E
APPLICANT: Goristan, Mary E
APPLICANT: Godoski, Paul J
APPLICANT: Godoski, Paul J
APPLICANT: Godoski, Paul J
APPLICANT: Godoski, Paul J
APPLICANT: Roy, Margaret Ann
APPLICANT: Napier, Mary A
APPLICANT: Napier, Mary A
APPLICANT: Tumas, Daniel
APPLICANT: William I
APPLICANT: William I
APPLICANT: William I
APPLICANT: Wood, William I
APPLICANT: Wood, William I
APPLICANT: Wood, William I
APPLICANT: Lang, Zemin
APPLICANT: Acids Encoding the Same
TILE OF INVENTION NUMBER: 00/04797
PRIOR APPLICATION NUMBER: 60/062250
PRIOR APPLICATION NUMBER: 60/062250
PRIOR APPLICATION NUMBER: 60/065186
PRIOR APPLICATION NUMBER: 60/065186
PRIOR APPLICATION NUMBER: 60/065186
PRIOR FILING DATE: 1997-01-12
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APPLICANT: Baker, Kevin P.

APPLICANT: Botstein, David

APPLICANT: Botstein, David

APPLICANT: Desnoyers, Luc

APPLICANT: Eaton, Dan L.
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US-09-991-163-407
; Sequence 407, Ap
; Patent No. US200
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Best Local Similarity 99.4%;
Matches 310; Conservative
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PRIOR APPLICATION NUMBER: 60/092182
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| PRIOR APPLICATION NUMBER: 60/065311 | PRIOR FILING DATE: 1997-11-13 | PRIOR FILING DATE: 1997-11-13 | PRIOR FILING DATE: 1997-11-24 | PRIOR PRIOR FILING DATE: 1998-03-20 | PRIOR FILING DATE: 1998-03-20 | PRIOR FILING DATE: 1998-03-20 | PRIOR FILING DATE: 1998-05-07 | PRIOR PRIOR FILING DATE: 1998-05-07 | PRIOR PRIO

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RESULT 13
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Patent N
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Best Local Similarity 99.4%;
Matches 310; Conservative
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OR FILING DATE: 1998-07-02
OR APPLICATION NUMBER: 60/091544
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OR APPLICATION NUMBER: 60/091626
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OR FILING DATE: 1998-07-02
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OR APPLICATION NUMBER: 60/091982
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US20020137075A1
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Fong, Sherman
Gerber, Hanspeter
Gerritsen, Mary E.
Goddard, Audrey
Godowski, Paul J.
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Baker, Kevin P.
Botstein, David
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ACAGTGTTTGGC 390
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Roy, Margaret Ann
Stewart, Timothy A.
Tumas, Daniel
Watanabe, Colin K.
Williams, P. Mickey
                                                                                                               Grimaldi, J. Christopher Gurney, Austin L.
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Eaton, Dan L.
                                                                                      Napier, Mary A.
                                                                                                    Kljavin, Ivar J.
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APPLICANT: Whod, William I.

APPLICANT: Sching. Scale and Transmembrane Polypeptides and Nucleic Title OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic Title OF INVENTION: Acids Encoding the Same

PILL REFERENCE: P27301025

PELL REFERENCE: P27301025

PELC RILLING DATE: 1997.06-16

PELC RAPLICATION NUMBER: 60,06518

PELC RAPLICATION NUMBER: 60,005311

PELC RAPLICATION NUMBER: 60,005111

PELC RAPLICATION NUMBER: 60,007545

PELC RILLING DATE: 1986.00-20

PELC RAPLICATION NUMBER: 60,007545

PELC RAPLICATION NUMBER: 60,008025

PELC RAPLICATION NUMBER:
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RESULT 14
US-09-990-456-407
; Sequence 407, Application US/09990456
; Patent NO. US20020137890A1
; GENERAL INFORWATION;
; APPLICANT: Ashkenazi,Avi J.
; APPLICANT: Baker, Kevin P.
; APPLICANT: Destsein,David
; APPLICANT: Destsein,David
; APPLICANT: Eaton,Dan L.
; APPLICANT: Ferrara,Napoleone
; APPLICANT: Ferrara,Napoleone
; APPLICANT: Gerber,Hanspeter
; APPLICANT: Gerber,Hanspeter
; APPLICANT: Gerritsen,Mary E.
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Best Local Similarity 99.4%;
Matches 310; Conservative
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OR APPLICATION NUMBER: 60/990694
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OR FILING DATE: 1998-06-26
OR FILING DATE: 1998-06-26
OR APPLICATION NUMBER: 60/990863
OR FILING DATE: 1998-06-26
OR APPLICATION NUMBER: 60/991360
OR FILING DATE: 1998-07-01
OR APPLICATION NUMBER: 60/091478
OR FILING DATE: 1998-07-02
OR APPLICATION NUMBER: 60/091519
OR FILING DATE: 1998-07-02
OR APPLICATION NUMBER: 60/091626
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PRIOR ADPLICATION NUMBER: 60/08858
PRIOR FILING DATE: 1998-06-11
PRIOR PHILICATION NUMBER: 60/088861
PRIOR PHILING DATE: 1998-06-11
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PRIOR APPLICATION NUMBER: 60/08976
PRIOR APPLICATION NUMBER: 60/08951
PRIOR APPLICATION NUMBER: 60/08953
PRIOR PHILING DATE: 1998-06-16
PRIOR APPLICATION NUMBER: 60/08953
PRIOR PHILING DATE: 1998-06-17
PRIOR APPLICATION NUMBER: 60/08959
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PRIOR PHILING DATE: 1998-06-17
PRIOR APPLICATION NUMBER: 60/08960
PRIOR PHILING DATE: 1998-06-17
PRIOR APPLICATION NUMBER: 60/08990
PRIOR PHILING DATE: 1998-06-17
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PRIOR PHILING DATE: 1998-06-22
PRIOR PHILING DATE: 1998-06-24
PRIOR PHILING DATE: 1998-

1998-0 1	APPLICANT: Goddwski, Paul J. APPLICANT: Goddwski, Paul J. APPLICANT: Grimaldi, J.Christopher APPLICANT: Gurney, Austin L. APPLICANT: Napier, Mary A. APPLICANT: Napier, Mary A. APPLICANT: Pan, James APPLICANT: Pan, James APPLICANT: Pan, James APPLICANT: Pan, James APPLICANT: Water Ann APPLICANT: Wood, William I. APPLICANT: Wood, Williams, P. Mickey APPLICANT: Wood, Williams I. APPLICANT : Wood, William I. APPLICANT: Wood, William I. APPLICANT : Wood, William I. APPLICANT : Wood, William I. APPLICANTON NUMBER: GO/049787 PRIOR APPLICATION NUMBER: US/09/990, 456 CURRENT FILING DATE: 1997-06-16 PRIOR APPLICATION NUMBER: 60/062250 PRIOR APPLICATION NUMBER: 60/062250 PRIOR APPLICATION NUMBER: 60/065186 PRIOR APPLICATION NUMBER: 60/065311 PRIOR APPLICATION NUMBER: 60/066311 PRIOR APPLICATION NUMBER: 60/066770 PRIOR APPLICATION NUMBER: 60/078910 PRIOR APPLICATION NUMBER: 60/083322
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	PRIOR FILING DATE: 1998-06-09 PRIOR APPLICATION NUMBER: 60/088734 PRIOR APPLICATION NUMBER: 60/088738 PRIOR APPLICATION NUMBER: 60/088738 PRIOR APPLICATION NUMBER: 60/088742 PRIOR APPLICATION NUMBER: 60/088810 PRIOR APPLICATION NUMBER: 60/088810 PRIOR APPLICATION NUMBER: 60/088810 PRIOR APPLICATION NUMBER: 60/088824 PRIOR APPLICATION NUMBER: 60/088826 PRIOR APPLICATION NUMBER: 60/088858 PRIOR FILING DATE: 1998-06-10 PRIOR APPLICATION NUMBER: 60/088861 PRIOR APPLICATION NUMBER: 60/088861 PRIOR APPLICATION NUMBER: 60/088876 PRIOR APPLICATION NUMBER: 60/089876 PRIOR FILING DATE: 1998-06-11 PRIOR APPLICATION NUMBER: 60/089105 PRIOR FILING DATE: 1998-06-12 PRIOR APPLICATION NUMBER: 60/089514 PRIOR APPLICATION NUMBER: 60/089514 PRIOR APPLICATION NUMBER: 60/089514 PRIOR APPLICATION NUMBER: 60/089514 PRIOR APPLICATION NUMBER: 60/089532 PRIOR APPLICATION NUMBER: 60/089532 PRIOR FILING DATE: 1998-06-16 PRIOR APPLICATION NUMBER: 60/089532 PRIOR APPLICATION NUMBER: 60/089532 PRIOR FILING DATE: 1998-06-17 PRIOR APPLICATION NUMBER: 60/089534 PRIOR APPLICATION NUMBER: 60/089539 PRIOR FILING DATE: 1998-06-17 PRIOR APPLICATION NUMBER: 60/089599 PRIOR APPLICATION NUMBER: 60/089599

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APPLICANI: APPLICATION: Secreted and Transmembrane Polypeptides and Nucleic TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic TITLE OF INVENTION: Acids Encoding the Same

FULL REFERENCE: P2730PLCS5

CURRENT FILING DATE: 1907-06-16

PRIOR APPLICATION UNMERS: 60/05250

PRIOR PRIOR PPLICATION UNMERS: 60/06250

PRIOR PPLICATION UNMERS: 60/06250

PRIOR PPLICATION UNMERS: 60/06250

PRIOR PPLICATION UNMERS: 60/065311

PRIOR PPLICATION UNMERS: 60/06570

PRIOR PPLICATION UNMERS: 60/075945

PRIOR APPLICATION UNMERS: 60/075945

PRIOR APPLICATION UNMERS: 60/083322

PRIOR APPLICATION UNMERS: 60/08700

PRIOR APPLICATION UNMERS: 60/08702

PRIOR APPLICATION UNMERS: 60/088021

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PRIOR PRICATION UNMERS: 60/088030

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GENERAL INFORMATION:
APPLICANT: Baker, Kevin P.
APPLICANT: Baker, Kevin P.
APPLICANT: Bestein, David
APPLICANT: Beston, Dan L.
APPLICANT: Ferrara, Napoleone
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Goddard, Audrey
Godowski, Paul J
Grimaldi, J.Christopher
Gurney, Austin L
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Stewart, Timothy A.
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OR APPLICATION NUMBER: 60/091696
OR FILING DATE: 1998-06-26
OR APPLICATION NUMBER: 60/091360
OR FILING DATE: 1998-07-02
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l: /cgn2_6/ptodata/2/pna/I
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Copyright (c) 1993 - 2003
"cqnn2_6/ptodata/2/pna/pcTUS_COMB.seq: *
(cgn2_6/ptodata/2/pna/pcTUS_COMB.seq: *
(cgn2_6/ptodata/2/pna/USO7_COMB.seq: *
(cgn2_6/ptodata/2/pna/USO7_COMB.seq: *
(cgn2_6/ptodata/2/pna/USO7_COMB.seq: *
(cgn2_6/ptodata/2/pna/USO80_COMB.seq: *
(cgn2_6/ptodata/2/pna/USO90_COMB.seq: *
(cgn2_6/
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Compugen Ltd
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45: //gnz_6/ptodata/2/pna//ISI01B_COMB.seq; 47: //gnz_6/ptodata/2/pna//ISI01B_COMB.seq; 47: //gnz_6/ptodata/2/pna//ISI01B_COMB.seq; 48: //gnz_6/ptodata/2/pna//ISI01B_COMB.seq; 48: //gnz_6/ptodata/2/pna//ISI01B_COMB.seq; 49: //gnz_6/ptodata/2/pna//ISI01B_COMB.seq; 53: //gnz_6/ptodata/2/pna//ISI01B_COMB.seq; 53: //gnz_6/ptodata/2/pna//ISI01B_COMB.seq; 55: //gnz_6/ptodata/2/pna//ISI001C_COMB.seq; 55: //gnz_6/ptodata/2/pna//ISI001C_COMB.seq; 56: //gnz_6/ptodata/2/pna//ISI001C_COMB.seq; 56: //gnz_6/ptodata/2/pna//ISI001C_COMB.seq; 56: //gnz_6/ptodata/2/pna//ISI0005C_COMB.seq; 56: //gnz_6/ptodata/2/pna//ISI0005C_COMB.seq; 56: //gnz_6/ptodata/2/pna//ISI0005C_COMB.seq; 56: //gnz_6/ptodata/2/pna//ISI0005C_COMB.seq; 56: //gnz_6/ptodata/2/pna//ISI0005C_COMB.seq; 56: //gnz_6/ptodata/2/pna//ISI0005C_COMB.seq; 57: //gnz_6/ptodata/2/pna//ISI01C_COMB.seq; 57: //
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.
Score
Query Score Match Length
В
DB ID
Description

240

180

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RESULT 1

PCT-US02-05403-3

Sequence 3, Application PC/TUS0205403

Sequence 3, Application PC/TUS0205403

Sequence 3, Application Institute, Inc.

APPLICANT: Dana-Farber: Cancer Institute, Inc.

PITLE PETERENCE: 00530-094801

CURRENT APPLICATION NUMBER: PCT/US02/05403

CURRENT FILING DATE: 2002-02-22

PRIOR APPLICATION NUMBER: 60/270,973

PRIOR FILING DATE: 2001-02-23

UMMBER OF SEQ ID NOS: 32

SOFTWARE: FASTSED for Windows Version 4.0

SEQ ID NO 3

LENGTH: 312
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                                                                                                      : LENGTH: 312
TYPE: DNA
: ORGANISM: Homo sapiens
PCT-USO2-05403-3
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                                     Query Match
Best Local Similarity
Matches 312; Conserv
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                                          ALIGNMENTS
                                                                         Length 312;
                                            Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Sequence 35, Appl
Sequence 179, App
Sequence 11845, A
Sequence 11845, Appl
Sequence 6, Appli
Sequence 199, App
Sequence 199, App
Sequence 6, Appli
Sequence 6, Appli
Sequence 6, Appli
Sequence 8, Appli
Sequence 8, Appli
Sequence 8, Appli
Sequence 27, Appli
Sequence 407, App
                                            0;
                                            Gaps
                                              0
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(SENERAL INFORMATION:
APPLICANT: Polyak, Kornelia
APPLICANT: Polyak, Kornelia
APPLICANT: Sgroi, Dennis
APPLICANT: Sgroi, Dennis
APPLICANT: Krop, Ian
TITLE OF INVENTION: HIN-1, A TUMOR SUPPRESSOR GENE
FILE REFERENCE: 00530-094001
(CURRENT APPLICATION NUMBER: US/10/081,817
(CURRENT APPLICATION NUMBER: 60/270,973
(CURRENT FILING DATE: 2001-02-23
(CURRENT FILING DATE: 2001-02-23
(CURRENT APPLICATION NUMBER: 60/251,908
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US-10-081-817-3
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Best Local Similarity
Matches 312; Conserv
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121 GAGGCCGGGGCCCGGGACCCTGGCCAACCCCTCAACCCGCTGAAGCTCCTG 180
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                                                             GAGCTGGGTCCCCAGGCCGTGGGGGGCCGTGAAGGCCCTGAAGGCCCTGCTGGGGGCCCTG
                                                                                                        CTGAGCAGCCTGGGCATCCCCGTGAACCACCTCATAGAGGGCTCCCAGAAGTGTGTGGCT
                                                                                                                       CTGAGCAGCCTGGGCATCCCCGTGAACCACCTCATAGAGGGCTCCCAGAAGTGTGTGGCT
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                                              GAGCTGGGTCCCCAGGCCGTGGGGGCCCTGAAGGCCCTGCTGCTGGGGGCCCTG
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RESULT 3
US-10-631-467
US-10-631-467
Sequence 467, Application US/10631467
Sequence 467, Application US/10631467
SEQUENCE INFORMATION:
APPLICANT: Genox Research Inc.
TITLE OF INVENTION: Method for testing for broncheal asthma, or chronic obstructive prints of Invention; disease
FILE REFERENCE: 3462.1005-000
CURRENT FAPALICATION NUMBER: US/10/631,467
CURRENT FILING DATE: 2003-07-31
PRIOR APPLICATION NUMBER: JP 2003-077212
PRIOR FILING DATE: 2003-03-03-09
PRIOR FILING DATE: 2003-03-20
PRIOR FILING DATE: 2003-03-20
PRIOR FILING DATE: 2002-08-06
NUMBER OF SEQ ID NOS: 2086
SOFTWARE: PAtentin version 3.1
SEQ ID NO 467
SEQ ID NO 46
                                                                                                                                                                                                                                                                                                                                                                            RESULT 4
US-09-489-036-35171
; Sequence 35171, Appli
; GENERAL INFORMATION:
; APPLICANT: Hyseq, In
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Best Local
                                                                                                                                                           CURRENT APPLICATION NUMBER: US/09/489,036
CURRENT FILING DATE: 2000-01-19
NUMBER OF SEQ ID NOS: 35324
SOFTWARE: Hy-patent.pl Version 3.1
SEQ ID NO 35171
                                                                                                                                                                                                                                                                                TITLE OF INVENTION: Novel Nucleic Acid Sequences Obtained TITLE OF INVENTION: From Various Libraries FILE REFERENCE: 783
                                                                                                           LENGTH: 44
TYPE: DNA
NAME/KEY: misc_feature LOCATION: (1)...(446)
                                                                            ORGANISM: Homo sapiens
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322 ACAGTGTTTGGC 333
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Conservative 0;
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Pred. No. 3.9e-46;
); Mismatches 0;
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APPLICANT: Hyseq, Inc.

APPLICANT: Hyseq, Inc.

TITLE OF INVENTION: Rovel Nucleic Acid Sequences Obt

TITLE OF INVENTION: From Various Libraries

FILE REFERENCE: 783

CURRENT APPLICATION NUMBER: US/09/943,143

CURRENT FILING DATE: 2001-08-30

PRIOR APPLICATION NUMBER: 09/489,036

PRIOR APPLICATION NUMBER: 09/489,036

PRIOR FILING DATE: 2000-01-19

NUMBER OF SED ID NOS: 35324

SOFTWARE: Hy-patent.pl Version 3.1

SEQ ID NO 35171

SEQ ID NO 35171

SEQ ID NO 35171

COGANUSM: Homo sapiens

FEATURE:

NAME/KBY: misc_feature

LOCATION: (1)...(446)

COCATION: (1)...(446)

COCATION: (1)...(446)

COCATION: (1)...(446)
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US-09-943-143-35171, Application US/09943143
Sequence 35171, Application US/09943143
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Best Local Similarity
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Matches
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nes 310; Conser
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   331 GAGCTGGGTCCCCAGGCCGTGGGGGCCGTGAAGGCCCTGAAGGCCCTGCTGGGGGCCCTG
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391 ACAGTGTTTGGC 402
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                                                                                 61 TTCTTAGTGGGCTCGGCCAAGCCTGTGGCCCAGCCTGTCGCTGCGCTGGAGTCGGCGGCG 120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     91 ATGAAGCTCGCCGCCCTCCTGCGGCCCTGTGCGTCCTGCAGCTCCGCTGCTGCT 150
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                                                                                                                                         ATGAAGCTCGCCGCCCTCCTGGGGCTCTGCGTGGCCCTGTCCTGCAGCTCCGCTCGTGCT
                         . GAGGCCGGGGCCGGGACCCTGGCCAACCCCTCGGCACCCTCAACCCGCTGAAGCTCCTG
CTGAGCAGCCTGGGCATCCCCGTGAACCACCTCATAGAGGGCTCCCAGAAGTGTGTGGCT
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ilarity 99.4%;
Conservative
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Pred. No. 1.
                                                                                                                                                                                                     Score 308.8; DB 40;
pred. No. 1.5e-45;
0; Mismatches 2;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Mismatches
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                                                             180
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                                270
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RESULT 7

US-09-710-281-179

Sequence 179, Application US/09710281

GENERAL INFORMATION:
APPLICANT: Hunter, John J.
APPLICANT: Styjan, Andrew W.
APPLICANT: Styjan, Andrew W.
APPLICANT: Styjan, Andrew W.
TITLE OF INVENTION: NOVEL NUCLEIC ACID MOLECULES AND TITLE OF INVENTION: THEREFOR FILLE REFERENCE: 1600.2036-001

CURRENT APPLICATION NUMBER: US/09/710,281
CURRENT FILING DATE: 2000-11-10
PRIOR APPLICATION NUMBER: 60/164,254
PRIOR FILING DATE: 1999-11-09
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; ORGANISM: Human
US-60-449-155-36
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US-60-449-155-36
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GENERAL INFORMATION:
APPLICANY: Keith, Tim
APPLICANION: RELATING TO RESPIRATORY DISEASES AND AMINO ACID SEQUENCES
TITLE OF INVENTION: RELATING TO RESPIRATORY DISEASES AND AMINO ACID SEQUENCES TIP
CURRENT FILLING DATE: 2003-02-20
CURRENT FILLING DATE: 2003-02-20
NUMBER OF SEQ ID NOS: 1000
SOFTWARE: FASTSEQ FOR Windows Version 4.0
SEQ ID NO 36
LENGTH: 461
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Best Local Similarity 199.4%;
Matches 310; Conservative
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US-10-170-235-38638
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                                                                                                                                                                                                                                                                           Sequence 38638, Application US/10170235

GENERAL INFORMATION:
APPLICANT: VENYER, J. Craig
TITLE OF INVENTION: KITS, SUCH AS NUCLEIC ACID ARRAYS, COMPRISING A MAJORITY OF HU
TITLE OF INVENTION: TRANSCRIPTS, FOR DETECTING EXPRESSION AND OTHER USES THEREOF
FILE REFERENCE: CL001380
CURRENT APPLICATION NUMBER: US/10/170,235
CURRENT FILING DATE: 2003-03-17
NUMBER OF SEQ ID NOS: 42514
SEQ ID NO 38638
LENGTH: 469
TYPE: DNA
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Best Local Sim
Matches 310;
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SOFTWARE: FastSEQ for Windows Version
SEQ ID NO 179
LENGTH: 467
TYPE: DNA
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Best Local Similarity
Matches 310; Conserv
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352 ACAGTGTTTGGC 363
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172 GAGGCCGGGGCCGGGACCCTGGCCAACCCCTCGGCACCCTCAACCCGCTGAAGCTCCTG 231
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 CTGAGCAGCCTGGGCATCCCCGTGAACCACCTCATAGAGGGCTCCCCAGAAGTGTGTGGCT
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ilarity 99.4%;
Conservative (
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Pred. No. 1.5e-45;
0; Mismatches 2;
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Pred. No. 1.5e-45;
0; Mismatches 2;
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; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: (1)...(491)
; OTHER INFORMATION: n = A,T,C or
US-09-277-227-11845
RESULT 10
US-09-346-956-15624
US-09-346-956-15624
Sequence 15024, Application US/09346956
GENERAL INFORMATION:
APPLICANT: HYSEQ, Inc.
TITLE OF INVENTION: NOVEL NUCLEIC ACID SEQUENCES OBTAINED TITLE OF INVENTION: FROM VARIOUS CDNA LIBRARIES
FILE REFERENCE: 20411-758CON1
CURRENT APPLICATION NUMBER: US/09/346,956
CURRENT FILING DATE: 1999-07-02
EARLIER APPLICATION OMBER: US 09/210,298
FEARLIER APPLICATION OMBER: US 09/210,298
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Best Local S
Matches 310
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APPLICANT: Hyseq, Inc.
APPLICANT: HYSEQ, INC.
TITLE OF INVENTION: FOOM VARIOUS CDNA LIBRARIES
FILE REFERENCE: 20411-766
CURRENT FILMS DATE: 199-03-25
CURRENT FILMS DATE: 199-03-25
NUMBER OF SEQ ID NOS: 23680
SOFTWARE: FRASTSEQ for Windows Version 3.0
SEQ ID NO 11845
LENGTH: 491
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mes 310; Conserv
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Pred. No. 1.4e-45;
0; Mismatches 2; Indels 0;
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Sequence 15624, Application US/09904703

GENERAL INFORMATION:
APPLICANT: Hyseq, Inc.
TITILE OF INVENTION: NOVEL NUCLEIC ACID SEQUENCES OBTITILE OF INVENTION: FROM VARIOUS CDNA LIBRARIES
FILE REFERENCE: 20411-758CON1
CURRENT APPLICATION NUMBER: US/09/904,703
CURRENT FILING DATE: 2001-07-12
PRIOR APPLICATION NUMBER: 09/210,298
PRIOR APPLICATION NUMBER: 09/210,298
PRIOR FILING DATE: 1998-12-09
NUMBER OF SEQ ID NOS: 17812
SOFTWARE: FastSEQ for Windows Version 3.0
LENGTH: 491
TYPE: DNA
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                                                                                      ; FEATURE: misc_feature NAME/KEY: misc_feature; LOCATION: (1)...(491); OTHER INFORMATION: n - US-09-904-703-15624
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US-09-904-703-15624
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; LOCATION: (1)...(491)
; OTHER INFORMATION: n =
US-09-346-956-15624
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Best Local S
Matches 310
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Best Local Similarity
Matches 310; Conserv
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SOFTWARE: FASTSEQ for Windows Version
SEQ ID NO 15624
LENGTH: 491
                                                                                                                                          TYPE: DNA
ORGANISM: Homo sapiens
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ORGANISM: Homo sapiens
FEATURE:
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ATGAAGCTCGCCGCCCTCCTGGGGCTCTGCGTGCCTGTCCTGCAACCTCCGCTGCTGCT 120
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ACAGTGTTTGGC 372
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                                            Score 308.8;
Pred. No. 1.4e
0; Mismatches
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Pred. No. 1.4;
0; Mismatches
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GENERAL INFORMATION:
APPLICANT: Hyseq, Inc.
APPLICANT: Hyseq, Inc.
TITLE OF INVENTION: RROM VARIOUS cDNA LIBRARIES
FILE REFERENCE: 20411-766
CURRENT APPLICATION NUMBER: US/09/909,627
CURRENT FILING DATE: 2001-07-19
PRIOR APPLICATION NUMBER: 09/277,227
RRIOR FILING DATE: 1999-03-23
NUMBER OF SEQ ID NOS: 23680
SOFTWARE: FastSEQ for Windows Version 3.0
SOFTWARE: FastSEQ for Windows Version 3.0
FORGALISM: Homo Sapiens
FEATURE:
NAME/KEY: misc_feature
LOCATION: (1):..(491)
OTHER INFORMATION: n = A,T,C or G
US-09-909-627-11845
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US-09-909-627-11845
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Best Local S
Matches 310
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GENERAL INFORMATION:
APPLICANT: Hyseq, Inc.
                       361
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TPCTTAGTGGGCTCGGCCAAGCCTGTGGCCCAGCCTGTCGCTGGAGTCGGCGCGGGATTCGTCGCCGCG
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                                                                                                                                   GAGCTGGGTCCCCAGGCCGTGGGGGCCCTGAAGGCCCTGAAGGCCCTGCTGGGGGCCCTGCAAGGCCCTGCAGGCCCTGCAGGCCCTGCAGGCCCTGCAGGCCCTGCAGGCCCTGCAGGCCCTGCAGGCCCTGCTGGGGGCCCTTGAAGGCCCTTGAAGGCCCTTGCTGGGGGCCCTTGAAGGCCCTTGAAGGCCCTTGCTGGGGGGCCCTTGAAGGCCCTTGAAGGCCCTTGCTGGGGGGCCCTTGAAGGCCCTTGAAGGCCCTTGAAGGCCCTTGAAGGCCCTTGCTGGGGGGCCCTTGAAGGCCCTTGAAGGCCCTTGCTGGGGGGCCCTTTGAAGGCCCTTGAAGGCCCTTGAAGGCCCTTGAAGGCCCTTGAAGGCCCTTGCTGGGGGGCCCTTTGAAGGCCCTTGAAGGCCCTTGAAGGCCCTTGCTGGGGGGCCCTTTTGAAGGCCCTTGAAGGCCCTTGAAGGCCCTTGAAGGCCCTTGAAGGCCCTTGAAGGCCCTTGAAGGCCCTTGAAGGCCCTTGAAGGCCCTTGAAGGCCCTTGAAGGCCCTTGAAGGCCCTTGAAGGCCCTTGAAGGCCCTTGAAGGCCCTTGAAGGCCCTTGAAGGCCCTTGAAGGCCCTTGAAGGCCCTTGAAGGCCCTTGAAGGCCCTTGAAGGCCCTTGAAGGCCCTTGAAGGCCCTTGAAGGCCCTTGAAGGCCCTTGAAGGCCCTTGAAGGCCCTTGAAGGCCCTTGAAGGCCCTTGAAGGCCCTTGAAGGCCCTTGAAGGCCCTTGAAGGCCCTTGAAGGCCCTTGAAGGCCCTTGAAGGCCCTTGAAGGCCCTTGAAGGCCCTTGAAGGCCCTTGAAGGCCCTTGAAGGCCCTTGAAGGCCCTTGAAGGCCCTTGAAGGCCCTTGAAGGCCCTTGAAGGCCCTTGAAGGCCCTTGAAGGCCCTTGAAGGCCCTTGAAGGCCCTTGAAGGCCCTTGAAGGCCCTTGAAGGCCCTTGAAGGCCCTTGAAGGCCCTTGAAGGCCCTTGAAGGCCCTTGAAGGCCCTTGAAGGCCCTTGAAGGCCCTTGAAGGCCCTTGAAGGCCCTTGAAGGCCCTTGAAGGCCCTTGAAGGCCCTTGAAGGCCCTTGAAGGCCCTTGAAGGCCCTTGAAGGCCCTTGAAGGCCCTTGAAGGCCCTTGAAGGCCCTTGAAGGCCCTTGAAGGCCCTTGAAGGCCCTTGAAGGCCCTTGAAGGCCCTTGAAGGCCCTTGAAGGCCCTTGAAGGCCCTTGAAGGCCCTTGAAGGCCCTTGAAGGCCCTTGAAGGCCCTTGAAGGCCCTTGAAGGCCCTTGAAGGCCCTTGAAGGCCCTTGAAGGCCCTTGAAGGCCCTTGAAGGCCCTTGAAGGCCCTTGAAGGCCCTTGAAGGCCCTTGAAGGCCCTTGAAGGCCCTTGAAGGCCCTTGAAGGCCCTTGAAGGCCCTTGAAGGCCCTTGAAGGCCCTTGAAGGCCCTTGAAGGCCCTTGAAGGCCCTTGAAGGCCCTTGAAGGCCCTTGAAGGCCCTTGAAGGCCTTGAAGGCCCTTGAAGGCCCTTGAAGGCCCTTGAAGGCCCTTGAAGGCCCTTGAAGGCCCTTGAAGGCCCTTGAAGGCCCTTGAAGGCCCTTGAAGGCCCTTGAAGGCCCTTGAAGGCCCTTGAAGGCCCTTGAAGGCCCTTGAAGGCCCTTGAAGGCCCTTGAAGGCCCTTGAAGGCCCTTGAAGGCCCTTGAAGGCCCTTGAAGGCCCTTGAAGGCCCTTGAAGGCCCTTGAAGGCCCTTGAAGGCCCTTGAAGGCCCTTGAAGGCCCTTGAAGGCCCTTGAAGGCCCTTGAAGGCCCTTGAAGGCCCTTGAAGGCCCTTGAAGGCCCTTGAAGGCCCTTGAAGGCCCTTGAAGGCCCTTGAAGGCCCTTGAAGGCCCTTGAAGGCCCTTGAAGGCCCTTGAAGGCCCTTGAAGGCCCTTGAAGGCCCTTGAAGGCCCTTGAAGGCCCTTGAAGGCCCTTGAAGGCCCTTGAAGGCCCTTGAAGGCCCTTGAAGGCCCTTGAAGGCCCTTG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            CTGAGCAGCCTGGGCATCCCCGTGAACCACCTCATAGAGGGCTCCCCAGAACTGTGTGGCT
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                                                                           312
                          372
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Pred. No. 1.4e-45
0; Mismatches
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Sequence 10199, Application US/09471275

GENERAL INFORMATION:

APPLICANT: Hyseq, Inc.

TITLE OF INVENTION: NOVel Contigs Obtained

TITLE OF INVENTION: From Various Libraries

FILE REFERENCE: 782

CURRENT FILING DATE: 1999-01-20

EARLIER APPLICATION NUMBER: US 09/235,076

EARLIER APPLICATION NUMBER: US 09/234,611

EARLIER FILING DATE: 1999-01-20

EARLIER FILING DATE: 1999-01-20

EARLIER FILING DATE: 1999-01-20

EARLIER APPLICATION NUMBER: US 09/240,371

EARLIER FILING DATE: 1999-01-20

EARLIER APPLICATION NUMBER: US 09/277,227

EARLIER APPLICATION NUMBER: US 09/277,227

EARLIER APPLICATION NUMBER: US 09/271,490

EARLIER APPLICATION NUMBER: US 09/271,490

EARLIER FILING DATE: 1999-03-25

EARLIER APPLICATION NUMBER: US 09/274,861

EARLIER APPLICATION NUMBER: US 09/293,972

EARLIER APPLICATION NUMBER: US 09/293,972

EARLIER APPLICATION NUMBER: US 09/293,972

EARLIER APPLICATION NUMBER: US 09/296,350

EARLIER APPLICATION NUMBER: US 09/306,350

EARLIER FILING DATE: 1999-03-19

EARLIER FILING DATE: 1999-09-21

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            NAME/KEY: misc_feature; LOCATION: (443)...(20)
THER INFORMATION: similar to g1575322 in the genepept database; OTHER INFORMATION: Run with FASTXY 3.3t00, default parameters US-09-471-275-10199
                                                                                                                                                                                                                                                                                                                                                                                                                                               Query Match
Best Local S
Matches 310
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LOCATION: (1)...(513)
OTHER INFORMATION: n =
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ORGANISM: Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         FEATURE:
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                                                 181
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                                                                                                                                          GAGGCCGGGGCCGGGACCCTGGCCAACCCCCTCGGCACCCTCAACCCGCTGAAGCTCCTG
                                                                                                                                                                                                                                                   TTCTTAGTGGGCTCGGCCAAGCCTGTGGCCCAGCCTGTCGCTGCGCTGGAGTCGGCGGCG
                       CTGAGCAGCCTGGGCATCCCCGTGAACCACCTCATAGAGGGCTCCCAGAAGTGTGTGGCT
                                                                                                         GAGGCCGGGGCCCTGGCCAACCCCTCGGCACCCTCAACCCGCTGAAGCTCCTG
CTGAGCAGCCTGGGCATCCCCGTGAACCACCTCATAGAGGGCTCCCAGAAGTGTGTGGCT
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Gaps

393

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213

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release 114

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Sequence 495, Application US/09488725B
GENERAL INFORMATION:
APPLICANT: Yuanhua T. Tang
APPLICANT: John Tillinghast
APPLICANT: Ankura Sinku
APPLICANT: Chenghua Liu
APPLICANT: Chenghua Liu
APPLICANT: Radoje T. Drmanac
TITLE OF INVENTION: Novel Contigs Obtained
TITLE OF INVENTION: From Various Libraries
FILE REFERENCE: 784
                                                                                                                                                                                                                                                                                        PEATURE:

NAME/KEY: misc_feature

LOCATION: (1)...(513)

OTHER INFORMATION: n = a,t,c or g

FEATURE:

NAME/KEY: misc_feature

LOCATION: (75)...(496)

OTHER INFORMATION: similar to gi575322 in the genepept database release 114,

OTHER INFORMATION: Run with FASTXY 3.3t00, default parameters

US-09-488-725B-495
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 CURRENT APPLICATION NUMBER: US/09/488.725B
CURRENT EILING DATE: 2000-01-21
PRIOR APPLICATION NUMBER: US 09/004,182
PRIOR FILLING DATE: 1998-01-07
PRIOR FILLING DATE: 1998-02-13
PRIOR FILLING DATE: 1998-02-13
PRIOR PRICING DATE: 1998-02-13
PRIOR PRICING DATE: 1998-03-20
PRIOR PRICING DATE: 1998-03-20
PRIOR APPLICATION NUMBER: US 09/321,214
PRIOR APPLICATION NUMBER: US 09/321,214
PRIOR APPLICATION NUMBER: US 09/31,598
PRIOR APPLICATION NUMBER: US 09/131,598
PRIOR FILLING DATE: 1998-08-10
PRIOR PRICING DATE: 1998-10-13
PRIOR APPLICATION NUMBER: US 09/170,294
PRIOR APPLICATION NUMBER: US 09/179,473
PRIOR APPLICATION NUMBER: US 09/181,430
PRIOR APPLICATION NUMBER: US 09/181,430
PRIOR APPLICATION NUMBER: US 09/235,076
PRIOR APPLICATION NUMBER: US 09/235,076
PRIOR APPLICATION NUMBER: US 09/234,611
PRIOR PRIOR PRILING DATE: 1999-01-20
PRIOR FILLING DATE: 1999-01-20
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US-09-488-725B-495
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NUMBER OF SEQ ID NOS: 10289
SOFTWARE: pt_CT_genes Version 1.01
SEQ ID NO 495
LENGTH: 512
                                                                                                                                                                                                Matches
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Best Local
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ORGANISM: Homo sapiens
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ACAGTGTTTGGC 141
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                                                                                                                                                                                       Score 308.8; DB 21; Pred. No. 1.4e-45; 0; Mismatches 2;
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US-08-791-710-4
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                                                                                                                                                                                                                                                                                                              INFORMATION FOR SEQ ID NO: 4
SEQUENCE CHARACTERISTICS:
LENGTH: 518 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Sequence 4, Application US/08791710
GEMERAL INFORMATION:
APPLICANT: RUSSell, John C.
APPLICANT: COLPITTS, Tracey L.
TITLE OF INVENTION: REAGENTS AND METHODS FOR DETECTING TITLE OF INVENTION: LUNG DISEASES
NUMBER OF SEQUENCES: 12
CORRESPONDENCE ADDRESS:
ADDRESSE: ADDRESS: ADDRESSE: ADDR
                                                                                                                                                                                             Query Match
Best Local S
Matches 310
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FILING DATE:
FILING DATE:
ATTORNEY/AGENT INFORMATION:
NAME: POISMAND: PILSCILLA E.
REGISTRATION NUMBER: 3207
REFERENCE/DOCKET NUMBER: 5998.[
TELECOMMUNICATION INFORMATION:
THIEDHONE: 1847-937-0378
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        COMPUTER READABLE FORM:

MEDIUM TYPE: Diskette

COMPUTER: IBM Compatible

OPERATING SYSTEM: DOS

SOFTWARE: FastSEQ Version 2.0

CURRENT APPLICATION DATA:

APPLICATION UMBER: US/08/791,710

FILING DATE:

CLASSIFICATION UMBER:

APPLICATION NUMBER:

PRIOR APPLICATION NUMBER:
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CITY: Abbott Park
STATE: IL
COUNTRY: USA
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310; Conser
                                                                                             ACAGTGTTTGGC 312
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                                                                                                                                                                                       99.0%;
ilarity 99.4%;
Conservative
                                                                                                                                                                                       Score 308.8;
Pred. No. 1.4e
0; Mismatches
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1.4e-45;
                                                                                                                                                                                                                                        Length
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44, Appl
23253, A
30359, A
30359, A
31, Appl
32, Appl
1447, Appl
1447, Appl
1477, Appl
1737, Ap
24020, A
24020, A
24020, A
25, Appl
26, Appl
27, Appl
27, Appl
28, Appl
29, Appl
20, Ap

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Title:
Perfect score:
Sequence:
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Maximum DB seq length: 2000000000
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Maximum Match 100%
Listing first 45 summaries
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score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.
  Score
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          nucleic search, using sw model
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Match Length
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| cgn2_6/ptodata/1/pna/PcT_NEW_COMB.seq:*
| cgn2_6/ptodata/1/pna/US06_NEW_COMB.seq:*
| cgn2_6/ptodata/1/pna/US07_NEW_COMB.seq:*
| cgn2_6/ptodata/1/pna/US08_NEW_COMB.seq:*
| cgn2_6/ptodata/1/pna/US09_NEW_COMB.seq:*
| cgn2_6/ptodata/1/pna/US09_NEW_COMB.seq:*
| cgn2_6/ptodata/1/pna/US09_NEW_COMB.seq:*
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                                                                     atgaagctcgccgccctcct......gggccctgacagtgtttggc 312
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US-10-081-817A-26
US-10-081-817A-26
US-10-081-817A-26
US-10-081-817A-26
US-10-081-817A-26
US-10-081-817A-26
US-10-081-817A-26
US-09-475-704A-7
US-60-487-610-739
US-09-475-704A-9
US-10-425-114A-19
US-10-425-114A-10
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3 7 Appl

4 Appl

3 7 Appl

3 7 Appl

3 7 Appl

4 Appl

3 7 Appl

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Sequence 3, Application US/10081817A
GENERAL INFORMATION:
APPLICANT: Polyak, Kornelia
APPLICANT: Porter, Dale
APPLICANT: Sgroi, Dennis
APPLICANT: Sgroi, Dennis
APPLICANT: Sgroi, Dennis
APPLICANT: Krop, Ian
TITLE OF INVENTION: HIN-1, A TUMOR SUPPRESSOR GEN
FILE REFERENCE: 00530-094001
CURRENT APPLICATION NUMBER: US/10/081,817A
CURRENT FILING DATE: 2002-02-22
PRIOR APPLICATION NUMBER: US 60/270,973
PRIOR APPLICATION NUMBER: US 60/351,908
PRIOR APP
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Best Local Similarity
Matches 312; Conserv
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121 GAGGCCGGGGACCCCTGGCCAACCCCTCGGCACCCTCAACCCGCTGAAGCTCCTG 180
                                                                                                                                                                                                                                                    GAGCTGGGTCCCCAGGCCGTGGGGGCCGTGAAGGCCCTGAAGGCCCTGCTGGGGGCCCTG
            ACAGTGTTTGGC 312
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US-60-494-568-16
US-10-425-114A-33253
US-10-425-114A-30359
US-60-487-610-33
US-60-487-610-32
US-60-487-610-32
US-10-425-114A-147
US-10-355-238-1
US-10-425-114A-1737
US-10-425-114A-21616
US-10-425-114A-24020
US-10-369-983-8
US-10-369-983-8
US-10-369-983-6
US-10-369-983-6
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APPLICANT: POIYAK, KOTNELIA
APPLICANT: SGROI, Dennis
APPLICANT: SGROI, Dennis
APPLICANT: KTOP, Ian
ITILE OF INVENTION: HIN-1, A TUMOR SUPPRESSOR GENE
FILE REFERENCE: 00530-094001
CURRENT APPLICATION NUMBER: US/10/081,817A
CURRENT APPLICATION NUMBER: US 60/270,973
PRIOR APPLICATION NUMBER: US 60/270,973
PRIOR FILING DATE: 2001-02-23
PRIOR APPLICATION NUMBER: US 60/351,908
PRIOR FILING DATE: 2001-02-3
IPRIOR FILING DATE: 2001-0351,908
PRIOR FILING DATE: 2001-0351,908
PRIOR FILING DATE: 2001-05
SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 23
LENGTH: 252
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Sequence 4, Application US/10081817A
GENERAL INFORMATION:
APPLICANT: POLYAK, KOThelia
APPLICANT: POLYAK, KOThelia
APPLICANT: POLYAK, KOThelia
APPLICANT: STOL, Dahe
APPLICANT: STOL, Dahe
APPLICANT: KTOP, Ian
ITILE OF INVENTION: HIN-1, A TUMOR SUPPRESSOR GENE
FILE REFERENCE: 00530-094001
CURRENT APPLICATION NUMBER: US/10/081,817A
CURRENT FILING DATE: 2002-02-22
PRIOR APPLICATION NUMBER: US 60/270,973
PRIOR APPLICATION NUMBER: US 60/270,973
PRIOR FILING DATE: 2001-02-23
PRIOR APPLICATION NUMBER: US 60/351,908
PRIOR FILING DATE: 2002-01-25
SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 4
LENGTH: 258
TYPE: DNA
                                                                                                                                                                                                                                                                       RESULT 3
US-10-081-817A-23
Sequence 23, Application US/10081817A
GENERAL INFORMATION:
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US-10-081-817A-4
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Best Local Similarity
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ORGANISM: Homo sapiens
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           CTCCTGCTGAGCAGCCTGGGCATCCCCGTGAACCACCTCATAGAGGGCTCCCAGAAGTGT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ACAGTGTTTGGC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              | 82.7%; Score 258; DB 6; Length 25
| 11arity | 1100.0%; Pred. No. 2.5e-48;
| Conservative 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             312
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US-10-081-817A-7

Sequence 7, Application US/10081817A

GENERAL INFORMATION:
APPLICANT: Polyak, Kornelia
APPLICANT: Porter, Dale
APPLICANT: Porter, Dale
APPLICANT: Sgroi, Dennis
APPLICANT: Sgroi, Dennis
APPLICANT: Krop, Ian
ITILE OF INVENTION: HIN-1, A TUMOR SUPPRESSOR GENE
FILE REFERENCE: 00530-094001
CURRENT APPLICATION NUMBER: US/10/081,817A
CURRENT FILING DATE: 2002-02-22
PRIOR APPLICATION NUMBER: US 60/270,973
PRIOR APPLICATION NUMBER: US 60/270,973
PRIOR APPLICATION NUMBER: US 60/351,908
PRIOR FILING DATE: 2002-01-25

NUMBER OF SEO ID NOS: 32
SOFTWARE: FASTSEQ FOR Windows Version 4.0
SEQ ID NO 7
LENGTH: 312
TYPE: DNA
ORGANISM: Mus musculus
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                                                                                                                                                                                                                                                                             Query Match 34.7%; Score 108.2; DB 6; Length 312; Best Local Similarity 65.7%; Pred. No. 2.6e-15; Matches 190; Conservative 0; Mismatches 93; Indels 6
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Query Match
Best Local Similarity
Matches 252; Conserva
                   192
                               183 GAGCAGCCTGGGCATCCCCGTGAACCACCTCATAGAGGGCTCCCAGAAGTGTGTGGCTGA 242
                                                                        132 TGTGGCAGGGGCTGTGCCTAGCCTACCATTAAGCCACTTGGCCATCCTGAGGTTCATCCT
                                                                                                126 CGGGGCCGGGACCCTGGCCAAC---CCCCTCGGCACCCTCAACCCGCTGAAGCTCCTGCT 182
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   72 GACTCATTGGCCAAGCCTGCGGTAGAACCCGTGGCCGCTTGCTCCAGCTGCAGAGGC
                                                                                                                                                               301 ACAGTGTTTGGC 312
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    121 CTGAGCAGCCTGGGCATCCCCGTGAACCACCTCATAGAGGGCTCCCCAGAAGTGTGTGGCT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          241 ACAGTGTTTGGC 252
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   GGCCAGCATGGGCATCCCATTGGATCCTCTCATAGAGGGATCCAGGAAGTGTGTCACCGA
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Sequence 25. Application US/10081817A

GENERAL INFORMATION:
GENERAL INFORMATION:
APPLICANT: Polyak, Kornelia
APPLICANT: Portex, Dale
APPLICANT: Sgroi, Dennis
APPLICANT: Krop, Ian
TITLE OF INVENTION: HIN-1, A TUMOR SUPPRESSOR GENE
TITLE OF INVENTION: HUN-1, A TUMOR SUPPRESSOR GENE
TITLE OF INVENTION NUMBER: US/10/081,817A
CURRENT APPLICATION NUMBER: US/0/270,973
PRIOR APPLICATION NUMBER: US 60/270,973
PRIOR APPLICATION NUMBER: US 60/270,973
PRIOR FILING DATE: 2001-02-23
PRIOR FILING DATE: 2001-02-23
PRIOR APPLICATION NUMBER: US 60/351,908
PRIOR FILING DATE: 2002-01-25
NUMBER OF ESO ID NOS: 32
SOFTWARE: FastSEO for Windows Version 4.0
SETURN OF THE STATE OF THE 
                                                                              Sequence 8, Application US/10081817A

GENERAL INFORMATION:

APPLICANT: POLYAK, KOTNELIA

APPLICANT: POLYAK, KOTNELIA

APPLICANT: SGTOL, Dale

APPLICANT: STOL, IAN

APPLICANT: STOL, IAN

TITLE OF INVENTION: HIN-1, A TUMOR SUPPRESSOR GENE

TITLE OF INVENTION: HIN-1, A TUMOR SUPPRESSOR GENE

TITLE OF INVENTION NUMBER: US/10/081,817A

CURRENT FILLING DATE: 2002-02-22

PRIOR APPLICATION NUMBER: US 60/270,973

PRIOR APPLICATION NUMBER: US 60/270,973

PRIOR APPLICATION NUMBER: US 60/351,908

PRIOR APPLICATION NUMBER: US 60/351,908

PRIOR APPLICATION NUMBER: US 60/351,908

PRIOR FILING DATE: 2002-01-25

SOFTWARE: FRASTSEQ for Windows Version 4.0

SEQ ID NO 8

LENGTH: 255

TYPE: NAM
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; TYPE: DNA; ORGANISM: Mus musculus US-10-081-817A-8
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Query Match
Best Local :
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              124 ATCCTGGCCAGCATGGGCATCCCATTGGATCCTCTCATAGAGGGATCCAGGAAGTGTGTC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         178 CTGCTGAGCAGCCTGGGCATCCCCGGTGAACCACCTCATAGAGGGCTCCCAGAAGTGTGTG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              121 GAGGCCGGGGCCGGGACCCTGGCCAACCCCC---TCGGCACCCTTCAACCCGCTGAAGCTC 177
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    184
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       64 GAGGCTGTGGCAGGGGCTGTGCCTAGCCTACCATTAAGCCACTTGGCCATCCTGAGGTTC 123
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              249
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ACCGAGCTGGGCCCTGAGGCTGTAGGAGCTGTGAAGTCACTGCTGGGGGGTCCTG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           GCTGAGCTGGGTCCCCAGGCCGTGGGGGCCCTGAAGGCCCTGAAGGCCCTGCTG 291
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Pred. No. 2.6e-11;
); Mismatches 80
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          80; Indels
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Sequence 20, Application US/10081817A

GENERAL INFORMATION:
APPLICANT: Polyak, Kornelia
APPLICANT: Polyak, Kornelia
APPLICANT: Sgroi, Dale
APPLICANT: Sgroi, Dennis
APPLICANT: Krop, IAIN-1, A TUMOR SUPPRESSOR GENE
TITLE OF INVENTION: HIN-1, A TUMOR SUPPRESSOR GENE
TITLE OF INVENTION NUMBER: US/10/081,817A
CURRENT APPLICATION NUMBER: US/20/081,817A
CURRENT FILING DATE: 2002-02-22
PRIOR APPLICATION NUMBER: US 60/270,973
PRIOR APPLICATION NUMBER: US 60/270,973
PRIOR FILING DATE: 2001-02-23
PRIOR APPLICATION NUMBER: US 60/351,908
PRIOR FILING DATE: 2002-01-25
NUMBER OF ESG ID NOS: 32
SOFTWARE: FastSEQ for Windows Version 4.0
1 SEQ ID NO 20
1 TANGETH: 734
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US-10-081-817A-20
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Best Local Simi
Matches 151;
                                                                                                                                                                                                                                                                                                                                                                                                       ; TYPE: DNA; ORGANISM: Rattus norvegicus US-10-081-817A-20
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RESULT 8
US-10-081-817A-26
; Sequence 26, Application US/10081817A
; GENERAL INFORMATION:
; APPLICANT: POlyak, Kornelia
; APPLICANT: Porter, Dale
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                                                                                                                                        δÃ
                                                                                                                                                                          밁
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Matches
                                                                                                                                                                                                                                                                                                                                                              Query Match
Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                       TYPE: D
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              178 CTGCTGAGCAGCCTGGGCATCCCCGGTGAACCACCTCATAGAGGGCTCCCAGAAGTGTGTG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               121 GAGGCCGGGGCCGGGACCCTGGCCAACCCCC---TCGGCACCCTCAACCCGCTGAAGCTC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         190 ACCGAGCTGGGCCCTGAGGCTGTAGGAGGTCACTGCTGGGGGTCCTG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        238 GCTGAGCTGGGTCCCCAGGCCGTGGGGGGCCCTGAAGGCCCTGAAGGCCCTGCTG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              70
                                                                                                                                                                                                                                108 GGCTGTGCCTAGCCTAGCATTAAGCCACTTGGCCATCCTGAGGTTCATCGTGACCAGCCT 167
                                                                                                                                                                                                                                                 135 GACCCTGGCCAACCCCC---TCGGGACCCTCAACCCGCTGAAGCTCCTGCTGAGCAGCCT 191
                                                                                                                                                                                            228 TGAGGCTGTAGGAGCTGTGAAGTCACTGCTGGGGGCCCCTG
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                                                                                                                                           CCAGGCCGTGGGGGCCGTGAAGGCCCTGAAGGCCCCTGCTG 291
                                                                                                                                                                             Conservative
                                                                                                                                                                                                                                                                                                                                                    Conservative
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                                                                                                                                                                                                                                                                                                                                                                  28.0%;
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Pred. No. 2.6e-11; 
0; Mismatches 80; Indels
                                                                                                                                                                                                                                                                                                                                                  Score 87.4; DB 6;
Pred. No. 9.8e-11;
0; Mismatches 73;
                                                                                                                                                                                                                                                                                                                                                                                   Length 279;
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; APPLICANT: SGTO1, Denn1s
; APPLICANT: KrOp, Ian
; TITLE OF INVENTION: HIN-1, A TUMOR SUPPRESSOR GENE
; FILE REFERENCE: 00530-094001
; CURRENT APPLICATION NUMBER: US/10/081,817A
CURRENT APPLICATION NUMBER: US 60/270,973
; PRIOR APPLICATION NUMBER: US 60/251,903
; PRIOR FILING DATE: 2001-02-23
; PRIOR FILING DATE: 2002-01-25
; PRIOR APPLICATION NUMBER: US 60/351,908
; PRIOR FILING DATE: 2002-01-25
; NUMBER OF SEQ ID NOS: 32
; SOFTWARE: FASCEQ FOR Windows Version 4.0
; LEEGTH: 249
; TYPE: DNA
; ORGANISM: Rattus norvegicus
US-10-081-817A-26

127.9%; Score 87.2; DB 6;
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                                        Вb
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                                                                                                                          Qy
                                                                                                                                                                                                             TYPE: DNA

ORGANISM: HSV2

PCT-US03-11231-193
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; Sequence 193, Application
; GENERAL INFORMATION;
; APPLICATIF COTIAN COTPOR
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                                                                                                                                                                      Query Match
Best Local
                                                                                                                                                            Matches
                                                                                                                                                                                                                                                       APPLICANT: Day, Craig H.

APPLICANT: Hosken, Mancy A.

APPLICANT: PAISONS, JOSEPH M.

TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE DIAGNOSIS AND TITLE OF INVENTION: TREATMENT OF HERPES SIMPLEX VIRUS INFECTION FILE REFERENCE: 210121.53801PC

CURRENT FALLING DATE: 2003-04-09

RUMBER OF SEQ ID NOS: 267

SOFTWARE: FASTSEQ FOR Windows Version 4.0

DENOTH: 3957

TEVER: N. 1957
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                            127 GGGGCCGGGACCCTGGCCAACCCCCTCGGCACCCTCAACCCGCTGAAGCTCCTGCTGAGC 186
                                                                                                                                                        al Similarity
142; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           198 TGAGGCTGTAGGAGCTGTGAAGTCACTGCTGGGGGGCCCCTG 237
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           138
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    78
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                                                                                                       CTCGCCGCCTCCTGGGGCTCTGCGTGGGCTCGTGCTTTCTTA
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                                                                                                                                                   16.3%;
ilarity 48.3%;
Conservative
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                                                                                                                                                     0;
                                                                                                                                                Score 50.8; DB 1;
Pred. No. 0.017;
0; Mismatches 152;
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..le-10;
mes 73;
                                                                                                                                                                             Length 3957;
                                                                                                                                                 Indels
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RESULT 11
US-60-487-610-740
; Sequence 740, Application US/60487610
; GENERAL INFORMATION:
; APPLICANT: CARGILL, Michele
; APPLICANT: HUANG, Hongjin
                                                                                                                                                                                                                            В
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   CURRENT APPLICATION NUMBER: US/09/842,364A
CURRENT ETLING DATE: 2001-04-25
PRIOR APPLICATION NUMBER: US 09/599,362
PRIOR FILLING DATE: 2000-06-21
PRIOR PPLICATION NUMBER: US 60/141,032
PRIOR PPLICATION NUMBER: US 60/141,032
PRIOR FILLING DATE: 1999-06-25
PRIOR APPLICATION NUMBER: US 60/1699
PRIOR APPLICATION NUMBER: US 60/169,099
PRIOR FILLING DATE: 1999-12-20
PRIOR FILLING DATE: 1999-12-21
PRIOR FILLING DATE: 1999-13-21
PRIOR FILLING DATE: 1999-13-21
PRIOR APPLICATION NUMBER: US 60/113,686
                                                                                                                                                                                                                                                                                                                                                                                                                                                Query Match
Best Local S
Matches 110
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US-09-842-364A-10
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PRIOR FILING DATE: 1998-12-22
NUMBER OF SEQ ID NOS: 13
SOFTWARE: PATENTIN VERSION 3.2
SEQ ID NO 10
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          В
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GENERAL INFORMATION:
APPLICANT: Yen-Potin, Frances
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TITLE OF INVENTION: Apollooprotein A-IV-related Protein: Polypeptide, TITLE OF INVENTION: Sequences and Biallelic Markers Thereof FILE REFERENCE: G-089US04CIP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TYPE: DNA
ORGANISM: Human
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   APPLICANT:
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                                                                                                                                                        1002
                                                                                                                                                                                                                 138 CCTGGCCAACCCCCCCGGCACCCTCAACCCGCTGAAGCTCCTGCTGAGCAGCCTGGGCAT
                                                                                                                                                                                                                                                                                                                                                           822 CCAGCTTGAGGGCCTGACCTTCCAGATGAAGAAGAACGCCGAGGAGCTCAAGGCCAGGAT
                                                                                                                                                                                                                                                                                                                                                                                                                                          al Similarity 50.0
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         1466
                                                                                                                                                GGACCAGCAGGTGGAGGAGTTCCGACGCCGGGTGGAGCCC 1041
                                                                                                                                                                               CGTGGGGGCCGTGAAGGCCCTGCTGGGGGGCC 297
                                                                                                                                                                                                                                             CCCCGTGAACCACCTCATAGAGGGCTCCCAGAAGTGTGTGGCTGAGGCTGAGGCTCCCCAGGC 257
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Yen-Potin, Frances
Denison, Blake
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Dumas Milne Edwards, Jean-Baptiste
Duclert, Aymeric
Bouguelert, Lydie
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         GGTCCCCAGGCCGTGGGGGGCCCTGAAGGCCCTGCTGCTGGGGGCCCCTG 300
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                                                                                                                                                                                                                                                                                                                                                                                                                                     Score 44; DB 5; Length 1466;
Pred. No. 0.47;
0; Mismatches 110; Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                     Gaps
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                                                                                                                                                                                                                                                                                         941
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Sequence 7, Application US/09475704A

GENERAL INFORMATION:
APPLICANT: Barnett, Susan
APPLICANT: Zur Megede, Jan
TITLE OF INVENTION: POLYMUCLEOTIDES ENCODING ANTIGENIC HIV TYPI
TITLE OF INVENTION: POLYMUCLEOTIDES, POLYMEPTIDES AND USES THERE
FILLE REFERENCE: 1631.002
CURRENT APPLICATION NUMBER: US/09/475,704A
CURRENT FILING DATE: 1999-12-30
PRIOR APPLICATION NUMBER: 60/152,195
PRIOR APPLICATION SERVICES FOR FILING DATE: 1999-09-01
NUMBER OF SEQ ID NOS: 30
SODTWARE: Patentin Ver. 2.0
SEQ ID NO 7
LENGTH: 1944
TYPE: DNA
ORGANISM: Artificial Sequence
FEATURE:
OPHERE INFORMATION: Description of Autificial Contents
FEATURE:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Дb
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                                                                                                                                                                                                      ; OTHER INFORMATION: Description of Artificial Sequence: THER INFORMATION: gp140 coding region of HIV strain AUS-09-475-704A-7
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US-09-475-704A-7
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Best Local S
Matches 132
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TITLE OF INVENTION: LIVER FIBROSIS IN HEBEATITIS C VIRUS-INFECTED SUBJECTS,
TITLE OF INVENTION: METHODS OF DETECTION AND USES THEREOF
FILE REFERENCE: CL001469
CURRENT APPLICATION NUMBER: US/60/487,610
CURRENT FILING DATE: 2003-07-17
NUMBER OF SEQ ID NOS: 97101
SOFTWARE: FASTSEQ for Windows Version 4.0
SEQ ID NO 740
LENGTH: 1754
                                                                                                                                               Query Match
Best Local
                                                                                                                                Matches
                                                      1377
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CCAGCCTGTCGCTGCGCTGGAGTCGGCGGCGGGAGGCCGGGGGCCGGGACCCTGGCCAACCC
                                                      GGGTCCCCAGGCCGTGGGGGCCCTGAAGGCCCC 286
                                                                                       CGTGGCCCTGTCCAGCTCCGCTCGTGCTTTCTTAGTGGGCTCGGCCAAGCCTGTGGC
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                                                                                                                                               14.0%;
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                                                                                                                              Score 43.8; D
Pred. No. 0.54
D; Mismatches
                                                                                                                                                 . 54;
                                                                                                                                                               DB 5;
                                                                                                                                                                   Length 1944;
                                                                                                                                                                                                                         e: synthetic
AF110968
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US-60-487-610-739
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US-09-475-704A-8
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GENERAL INFORMATION:
APPLICANT: CARGILL, Michele
APPLICANT: HUANG, Hongiln
TITLE OF INVENTION: GENETIC POLYMORPHISMS ASSOCIATED WITH
TITLE OF INVENTION: LIVER FIBROSIS IN HEPATITIS C VIRUS-INFECTED SUBJECTS;
TITLE OF INVENTION: METHODS OF DETECTION AND USES THEREOF
FILE REFERENCE: CL001469
CURRENT APPLICATION NUMBER: US/60/487,610
CURRENT FILING DATE: 2003-07-17
NUMBER OF SEQ ID NOS: 97101
SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 739
LENGTH: 2425
Sequence 8, Application US/09475704A
GENERAL INFORMATION:
APPLICANT: Barnett, Susan
APPLICANT: PARTICLE OF INVENTION: POLYNGCLEOTIDES ENCODING ANTIGENIC TITLE OF INVENTION: POLYPEPTIDES, POLYPEPTIDES AND USE FILE REFERENCE: 1631.002
CURRENT APPLICATION NUMBER: US/09/475,704A
CURRENT FILING DATE: 1999-12-30
PRIOR APPLICATION NUMBER: 66/152,195
PRIOR APPLICATION UNMBER: 66/152,195
PRIOR FILING DATE: 1999-09-01
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Best Local S
Matches 132
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132; Conserv
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     GGCAGTCGAGGGAGCTGGGCCCCAAAGGCACCCAGGGTCC
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ilarity 47.0%;
Conservative
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Pred. No. 0.56;
L; Mismatches 148;
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Sequence 738, Application US/60487610

Sequence 738, Application US/60487610

GENERAL INFORMATION: Alchele
APPLICANT: CARGILL, Michele
APPLICANT: HUANG, HONGJIN
TITLE OF INVENTION: GENERIC POLYMORPHISMS ASSOCIATED WITH
TITLE OF INVENTION: LIVER FIBROSIS IN HEPATITIS C VIRUS-INFECTED SUBJECTS,
TITLE OF INVENTION: METHODS OF DETECTION AND USES THEREOF
FILL REFERENCE: CL001469
CURRENT APPLICATION NUMBER: US/60/487,610
CURRENT FILING DATE: 2003-07-17
NUMBER OF SEQ ID NOS: 97101
SEQ ID NOS: 97101
SED ID NO 738
LENGTH: 2480
TYPE: DNA
ORGANISM: Homo sapiens
US-60-487-610-738
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US-60-487-610-738
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Best Local Similarity 47.0%;
Matches 132; Conservative
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Best Local Similarity 47.6
Matches 129; Conservative
                                                                                                                                                                           1165 GCCCTCGGCCCACAAGGCCCCTCCCGGAGCCCCTGGTGTCCGAGGCCTTCCAGGGCCAGAAG 1224
                               1285 CGGGGTCCGGGAGGTGCCGMAGGCCCTAAGGGAGACCAGGGTATTGCAGGTTCCGACGGT 1344
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                                                                                                                                                                                                              6 GCTCGCCGCCCTCCTGGGGCTCTGCGTGCCTGTGCTGCAGCTCCGCTCGTGCTTTCTT 65
                                                                    CGGGGCCGGGACCCTGGCCAACCCCTCGGCACCCTCAACCCGCTGAAGCTCCTGCTGAG 185
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                CCTCGGCACCCTCAACCCGCTGAAGCTCCTGCTGAGCAGCCTGGGCATCCCCGTGAACCA 209
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           CCTGGGCGTGGCCCCACCGAGGCCCAAGCGCCGCGTGGTGGAGCGCGAGAAGCGCGCGT 1436
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Pred. No. 0.56;
1; Mismatches 148; Indels
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Q	Db	
246	1345	
24.5 CONTRACTOR ACCUPACTOR ACCUPA		

Search completed: September 20, 2003, 03:15:36 Job time: 64.46 secs

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1405 GGCAGTCGAGGGGAGCTGGGCCCCAAAGGCACCCAGGGTCC 1445

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Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries
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Maximum DB seq
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Perfect score:
Sequence:
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length: 2000000000
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312
1 atgaagctcgccgccctcct.....gggccctgacagtgtttggc 312
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Gapop 10.0 , Gapext 1.0
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1: gb_ba:
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gb_pl:*
gb_pl:*
gb_pr:*
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gb_sv:*
gb_sy:*
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em_bum:*
em_in:*
                              em_vi:*
em_htg_inv:*
em_htg_irv:*
em_htg_other:*
em_htg_pln:*
em_htg_pln:*
em_htg_prod:*
em_htg_rod:*
em_htg_mam:*
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em_ov:*
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em_om:*
em_htgo_hum:*
em_htgo_mus:*
em_htgo_other:*
 REFERENCE
AUTHORS
                                       RESULT 1
AY040564
LOCUS
DEFINITION
ACCESSION
VERSION
VERSION
KEYWORDS
SOURCE
ORGANISM
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Database :

Searched:

Run on: OM nucleic

score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

165.4 162.8 108.2 90.4 90.4 90.4 Score Query Match 100.0 228.3 211.1 1948 106873 156789 93872 853 147774 237587 303550 3957 154746 154746 154746 1575 166644 523 245659 283593 630 254981 130129 166777 168347 190024 127488 Length DB 10 6. 9 2210 10 10 AF313456 AF313457 AC131433 AF313457 AL606479 AL606479 AL606479 AL606479 AL606479 AF274959 AF274961 AF2749 AF313458 AC108083 AC106813 AC025336 AC122714 AC022095 BD082139 AY040564 AY040564 Homo sapi AF086152 Homo sapi BC029176 Homo sapi BC029176 Homo sapi BC029176 Homo sapi BD0821412 Reagents BD082141 Reagents AX201348 Sequence AX403520 Sequence AX403520 Sequence AX403520 Sequence AX7013458 Homo sapi AC1028031 Homo sapi AC1025134 Homo sapi AC102714 Homo sapi AC102714 Homo sapi AC102714 Homo sapi BD082139 Reagents AX334451 Sequence BC02131435 Rattus no AC1331435 Rattus no AF313459 Mus muscu AL606479 Mouse DNA BD082137 Reagents AX376116 Sequence BC024232 Homo sapi AX376176 Sequence BC021352 Homo sapi AX376176 Rattus no AF313459 Mus muscu AF274561 Mus muscu AF274561 Mus muscu AF27459 Mus muscu AF27459 Mus muscu AF27459 Mus muscu AF27451 Homo sapi AX358 Sequence 2 286099 Herpes simp Description

ALIGNMENTS

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleos Mammalla; Eutheria; Primates; Catarrhini; Hominidae; Homo. 1 (bases 1 to 461)
Krop, J.E., Sgroi, D., Porter, D.A., Lunetta, K.I., LeVangie, R., Sthh, P., Kaelin, C.M., Rhei, E., Bosenberg, M., Schnitt, S., Marks, J.R., Pagon, Z., Belina, D., Razumovic, J. and Polyak, K. AY040564 461 bp mRNA linear Homo sapiens HIN-1 putative cytokine mRNA, complete AY040564 GI:15079187 Homo sapiens (human) Euteleostomi; Homo. PRI 15-AUG-2001 cds.

Pred.

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312; Conser
Homo sapiens (human)
Homo sapiens (human)
Homo sapiens
Eukaryota, Metazoa, Chordata; Craniata; Vertebrata; Euteleostomi;
Eukaryota, Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Lotases, 1 to [471]
Woessner, J., Tan, F., Marra, M., Kucaba, T., Yandell, M., Martin, J.,
Marth, G., Bowles, L., Wylie, T., Bowers, Y., Steptoe, M., Thelsing, B.
Geisel, S., Allen, M., Underwood, K., Chappell, J., Person, B.,
                                                                                                                                                                                                                                                                                                                                                                                                                          61
                                                                                                                                                                                                                                                                                                                                                                                                                                            Homo sapiens full length AF086152 AF086152.1 GI:3483497 FLI_CDNA.
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                                                                                                                                                   HUMZB52D10
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Polyak, K., Króp, I. and Sgroi, D.
Direct Submission
Submitted (15-JUN-2001) Adult Oncology,
Submitted (15-JUN-2001) BJ40C, Boston,
Institute, 44 Binney St. D740C, Boston,
                                                                                                                                                                                                                                                      GAGCTGGGTCCCCAGGCCGTGGGGGCCCTGAAGGCCCTGAAGGCCCTGCTGGGGGGCCCTG
                                                                                                                                                                                                           ACAGTGTTTGGC 312
                                                                                                                                                                                                                                                                                                    CTGAGCAGCCTGGGCATCCCCGTGAACCACCTCATAGAGGGCTCCCAGAAGTGTGTGGCT
                                                                                                                                                                                                                                                                                                                                                                                                100.0%;
ilarity 100.0%;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         /organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           /product="HIN-1 putative cytokine"
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GTLANPLGTLNPLKLLLSSLGIPVNHLIEGSQKCVAELGPQAVGAVKALKALLGALTV
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cDNA clone
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MA 02115, USA
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121 GAGGCCGGGGCCGGGACCCTGGCCAACCCCCTCGGCACCCTCAACCCGCTGAAGCTCCTG
                                                                                       Genome Sequencing Center
Department of Genetics
washington University
St. Louis MO 63108, USA
http://genome.wustl.edu/gsc
mailto:est@watson.wustl.edu
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 NOTICE: This sequence represents the full insert of this cDNA. At attempt has been made to verify whether this corresponds to the full-length of the original mRNA from which it was derived. We have tried to obtain double-stranded, or double chemistry sequence across the entire clone, but potentially, there are areas in the sequence where this level of coverage was not achieved. Nevertheless, we are confident of the accuracy of this sequence as all regions of low quality, as defined by PHRAP (P. Green, in preparation), were visually inspected and edited accordingly. The consensus quality values for this sequence have been submitted
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Waterston,R.

Direct Submission
Submitted (24-AUG-1998) Department of Genetics, Washington
University, 4444 Forest Park Avenue, St. Louis, Missouri 63108, USA
SUBMITTED BY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Gibbons,M., Harvey,N., Pape,D., Chamberlain,A., Morales,R., Schurk,R., Ritter,E., Kohn,S., Swaller,T., Behymer,K., Hillier,L., Wilson,R. and Waterston,R.; Swaller,T., Behymer from Each Unigene Cluster
Unigene Cluster
Unpublished
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                                                                                                                                                                              GAGGCCGGGGCCCTGGCCAACCCCTCGGCACCCTCAACCCGCTGAAGCTCCTG
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                                                                                                                                                                                                                                                                          99.0%;
llarity 99.4%;
Conservative
                                                                                                                                                                                                                                                                                                                                                                            /mol_type="mRNA"
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/171 c 149 g 73 t
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Contact: MGC help desk
Email: dgapbs r@mail.nih.gov
Email: dgapbs r@mail.nih.gov
Tissue Procurement: Life Technologies, Inc.
cDNA Library Preparation: Life Technologies, Inc.
cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Baylor College of Medicine Human Genom
Sequencing Center
Sequencing Center
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 121
                                                                                                                                                al Similarity 99.4
310; Conservative
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Direct Submission

Direct Submission

Submitted (01-MAY-2002) National Institutes of Health, Mammalian Submitted (01-MAY-2002) National Cancer Gene Collection (MGC), Cancer Genomics Office, National Cancer Gene Collection (MGC), Cancer Genomics Office, National Cancer Institute, 31 Center Drive, Room 11A03, Bethesda, MD 20892-2590,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

1 (bases 1 to 503)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LINI at: http://image.llnl.gov Series: IRAK Plate: 50 Row: b Column: 24
This clone was selected for full length sequencing because it passed the following selection criteria: Hexamer frequency ORF analysis, Genomescan gene prediction.
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Gunaratne, P.H., García, A.M., Lu, X., Huly:
Yoon, V.S., Kowis, C.R., Lawrence, S., Mart
Richards, S., Gibbs, R.A.
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                           GAGGCCGGGGCCGGGACCCTGGCCAACCCCCTCGGCACCCTCAACCCGCTGAAGCTCCTG 180
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                                                                                                                                                                                                                                                                                                                                                                   /organism="Homo sapiens"
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                                                                                                                                                                                                                                                                                                                           codon_start=1
                                                                                                                                                                                                                                                                                                                                                     /note="Vector: pCMV-SPORT6"
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          GAGGCCGGGGCCGGGACCCTGGCCAACCCCCTCGGCACCCTCAACCCCCTGAAGCTCCTG
                                                                     JP 200152225-A/6
13-NCV-2001
30-JAN-1998 JP 1998533078
31-JAN-1997 US 08/791710
                                                                                                                                                                                        Conservative
                                                                                                                                                                                                                                                                 78
                                                                                                                                                                                                                                                                                                                          Location/Qualifiers
1. .519
                                                                                                                                                                                                                                                             /organism="Zea mays"
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190 c 170 g
                                                                                                                                                                                                      99.08;
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                                                                                                                                                                                      Score 308.8; DB 6; pred. No. 5.5e-39; 0; Mismatches 2;
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CTGAGCAGCCTGGGCATCCCCGTGAACCACCTCATAGAGGGCTCCCAGAAGTGTGTGGCT
                                                                                                                 GAGCTGGGTCCCCAGGCCGTGGGGGCCCTGAAGGCCCTGAAGGCCCTGCTGGGGGCCCTG 300
                                                                                                                                                                                                                 DNA linear PAT 27-AUG-2002 detecting diseases of the lung.
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Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; Liliopaida; Poales; Poaceae; PACCAD clade; Panicoideae; Andropogoneae; Zea.

1 (bases 1 to 519)

1 (bases 1 to 519)

Medel.P.A.B., Cohen,M., Colpitts,T.L., Friedman,P.N., Gordon,J., Granados,E.N., Hodges,S.C., Klass,M.R., Kratochvil,J.D., Rapp,L.R., Russell,J.C. and Stroupe,S.D.

Russell,J.C. and Stroupe,S.D.

Reagents and methods useful for detecting diseases of the lung Patent: JP 200152225-A 6 13-NOV-2001;
ABBOTT LABORATORIES I STROUPE C C12N15/63,C12N5/10,C12Q1/68,C07K14/47//C07K16/30,G01N33/574 CC Strandedness: Single; C Topology: Linear; N FRIEDMAN,
JULIAN GORDON, EDWARD N GRANADOS, STEVEN C HODGES, MICHAEL R JON D KRATOCHVIL, LISA ROBERTS RAPP, JOHN C RUSSELL, STEPHEN D PATRICIA A BILLING MEDEL, MAURICE COHEN, TRACEY L COLPITTS, PAULA Location/Qualifiers. PI

Length 519;

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Best Local Similarity
Matches 310; Conserv
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JOURNAL
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2E 1 (bases 1 to 562)

3S Medel, P.A. (Cohen, M., Colpitts, T.L., Friedman, P.N., Gordon, J., Granados, E.N.), Hodges, S.C., Klass, M.R., Kratochvil, J.D., Rapp, L.R., Russell, J.C. and Stroupe, S.D.

Reagents and methods useful for detecting diseases of the lung ABBOTT LABORATORIES
PN JP 200152225-A 5 13-NOV-2001;
PD 30-JAN-1998 JP 1998533078
PF 31-JAN-1997 US 08/791710
PI PATRICIA A BILLING MEDEL, MAURICE COHEN, TRACEY L COLPITTS, PAULA
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PI STRODE |
PC C12M15/63,C12N5/10,C12Q1/68,C07K14/47//C07K16/30,G01N33/574 CC
Strandedness: Single;
CC Topology: Linear;
FH Key Location/Qualifiers.
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      CTGAGCAGCCTGGGCATCCCCGTGAACCACCTCATAGAGGGCTCCCAGAAGTGTGTGGCT 240
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                                                                                                                                                                                           99.0%; Score 308.8; DB 6; Length 562; Ilarity 99.4%; Pred. No. 5.4e-39; Conservative 0; Mismatches 2; Indels 0
                                                                                                                                                                                                                                                                                                                                                                                                                               JULIAN GORDON, EDWARD N GRANADOS, STEVEN C HODGES, MICHAEL R
                                                                                                                                                                                                                                                                                                                                                                                                                                                      N FRIEDMAN
                                                                                                                                                                                                                                                            /organism="zea mays"
/mol_type="genomic DNA"
/db_xref="taxon:4577"
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VERSION
AR252648
Sequence 407 from patent
AR252648
AR252648.1 GI:27300556
                        570 bp E
407 from patent US 6478825.
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Db RESULT 7				Qу	Query Match Best Local Matches 31	FEATURES SOUTC SOUTC SOUTC SOUTC SOUTC	AUTHORS TITLE JOURNAL	E O	RESULT 6 AX201348 LOCUS DEFINITION ACCESSION VERSION KEYWORDS	Qу Db	Db	Db
379 ACAGTGTTTGGC 390	141 GAGCTGGGTCCCC	0-0	99	1 ATGAAGCTCGCCGCCCTCCTGGGGCTCTGCGTGGCCCTGTGCAGCTCCGCTCGTGCT 60	Match 99.0%; Score 308.8; DB 6; Length 569; ocal Similarity 99.4%; Pred. No. 5.4e-39; s 310; Conservative 0; Mismatches 2; Indels 0; Gaps 0;	Location/Qualifiers ce 1. 569 /organism="Homo sapiens" /mol_type="genomic DNA" /db_xref="taxon:9606" 128 a 190 c 170 g 81 t	Ashkenazi Hillan,K. Stone,D.M Compositi Patent: W Genentech	Homo sapiens (human) M Homo sapiens Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.	AX201348 N Sequence 27 from Patent WO0153486. AX201348 AX201348 AX201348.1 GI:15391167	301 ACAGTGTTTGGC 312 	241 GAGCTGGGTCCCCAGGCCGTGGGGGCCCTGAAGGCCCTGAAGGCCCTGCTGGGGGCCCTG 300 	

linear

PAT 20-DEC-2002

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KEYWORDS
SOURCE
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Unknown
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1 (bases 1 to 570)

1 (bases 1 to 570)

1 (bases 1 to 570)

Note: The implant of bone defects and use of the implant for the treatment of bone defects

Patent: US 6478825-A 407 12-NOV-2002;
                                                                                                                                                                                                                                                                                       379
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Similarity
                                                                                                                                                                                                                    AX403520 570 bp
Sequence 407 from Patent WO0073454.
AX403520
                                                                                           Ashkenazi,A.J., Baker,K.P., Botstein,D., Desnoyers,L., Eaton,D., Ferrara,N., Gerber,H., Gerritsen,M., Goddard,A., Godowskl,P., Grimaldi,C.J., Gurney,A.L., Kljavin,I., Napier,M.A., Pan,J., Panoni,N.F., Roy,M., Stewart,T.A., Tumas,D., Watanabe,C.K., Williams,P., Wood,W.I. and Zhang,Z. Secreted and transmembrane polypeptides and nucleic acids encoding
                                                                                                                                                             Homo sapiens (human)
Homo sapiens
Eukaryota, Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
                                                                                                                                                                                                             AX403520.1 GI:21437002
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ilarity 99.4%;
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1. 570
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  /organism="unknown"
190 c 170 g
                                                                           WO_0073454-A 407 07-DEC-2000;
             /organism="Homo sapiens"
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190 c 170 g
                                                          Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ; score 308.8; l; pred. No. 5.4e: 0; Mismatches
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Query Match
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   AF313458
Homo sapiens UGRP2 mRNA,
AF313458
AF313458.1 GI:16565421
                                                                                                                                                                                                                                                       2 (bases 1 to 347)
2 (bases 1 to 347)
Niimi,T., Copeland,N.G., Gilbert,D.J., Jenkins,N.A., Srisodsai,A., Niimi,T., Copeland,N.G., Gilbert,D.B., Keck-Waggoner,C.L., Popescu,N.C. and Kimura,S. Zimoniju, expression, and chromosomal localization of the mouse gene cloning, expression, and chromosomal localization of the mouse gene (sepbaal, alias Ugrp2) that encodes a member of the novel (sepbaal, alias Ugrp2) that encodes a member of the novel uteroglobin related protein gene family cytogenet. Genome Res. 97 (1-2), 120-127 (2002)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

1 (bases 1 to 347)

Nimi, T., Keck-Waggoner, C.L., Popescu, N.C., Zhou, Y., Levitt, R.C.
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ACAGTGTTTGGC 390
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Nimi, T. and Kimura, S.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Conservative
                                                                          /organism="Homo sapiens"
/mol_type="mRNA"
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11. 325
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/product="UGRP2"
/protein_id="AAL26217.1"
/protein_id="AAL26217.1"
/db_xref="Gi:16565422"
/translation="MKLAALLGLCVALSCSSAAAFLVGSAKPVAOPVAALESAAEAGA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            99.0%;
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Pred. No. 5.4
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BASE COUNT ORIGIN

45 ω

124

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118 g

GTLÅNPLGTLNPLKLLLSSLGIPVNHLIEGSQKCVAELGPQAVGAVKALKALLGALTV FG"

Query Match Best Local S Matches 309

Similarity

98.5%;

Conservative

309;

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Summary Statistics

Consensus quality: 124488 bases at least 040

Consensus quality: 128031 bases at least 020

Consensus quality: 128042 bases at least 020

Estimated insert size: 135000; agarcse-fp estimation

Estimated insert size: 135000; agarcse-fp estimation

Quality coverage: 7.66 in 020 bases; agarcse-fp estimation

Quality coverage: 7.97 in 020 bases; sum-of-contigs estimation

A NOTE: This is a 'working draft' sequence. It currently
                                                                                                                                                                                                                 Project Information
Center Project Name: 632820
Center clone name: CITB-H1_2013L15
                                                                                                                                                                                                                                                                                                                           Center: Joint Genome Institute
Center Code: JGI
Web site: http://www.jgi.doe.gov
                                                                                                                                                                                                                                         Direct Submission
Direct Submission
Submitted (25-JAN-2002) Production Sequencing Facility,
Genome Institute, 2800 Mitchell Drive, Walnut Creek, CA
                                                                                                                                                                                                                                                                                                                                                                                                                                     AC108083
HOMO sapiens chromosome 5 clone
SEQUENCE, 4 unordered pieces.
AC108083, AC108083
AC108083, GI118369929
HTG: HTGS_PHASE1; HTGS_DRAFT; HT
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Pred. No. 1.1e-38;
D; Mismatches 3;
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3 DRAFT
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94598, USA
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                                                                                   Mammalia; Butheria; Primates; C.

1 (bases 1 to 166777)

DOE Joint Genome Institute.
Sequencing of Human Chromosome 5
Unpublished
2 (bases 1)
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Direct Submission
Submitted (12-7AN-2002) Production Sequencing Facility, DOE Joint Genome Institute, 2800 Mitchell Drive, Walnut Creek, CA 94598, USA 3 (bases 1 to 166777)
DOE Joint Genome Institute.
                                                                   2 (bases 1 to 166777)
DOE Joint Genome Insti
                                                                                                                                                                            AC106813
GI:19224876
AC106813.3 GI:19224876
HTG; HTGS_PHASE2; HTGS_DRAFT;
HOMO sapiens (human)
Homo sapiens
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4421
23713
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48603
48703
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32397 c 30949 g 31146
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4420: gap of unknown length
23712: contig of 19292 bp in length
23812: gap of unknown length
48602: contig of 24790 bp in length
48702: gap of unknown length
130129: contig of 81427 bp in length
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Pred. No. 1.8e
0; Mismatches
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Center: Joint Genome Institute
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Center Project Name: 1519801
Center clone name: RPCI-11_586L9
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Similarity 98.8%;
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39804 c 41258 g 40888 t 200 others
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NRS Baitren, B., Linton, L., Nusbaum, C., Lander, E., Abraham, H., Allen, N.,

Baitren, B., Linton, L., Barna, N., Bastlen, V., Beda, F.,

Roder, B., Baldwin, J., Barna, N., Burkett, G.,

Campoplano, A., Castle, A., Choepel, V., Colangelo, M., Collins, S.,

Collymore, A., Cooke, P., Dearellano, K., Dewar, K., Diaz, J.S.,

Collymore, A., Cooke, P., Deyle, M., Ferreira, P., FitzHugh, W., Gage, D.,

Dodge, S., Domino, M., Doyle, M., Ferreira, P., TitzHugh, W., Gage, D.,

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Howland, J.C., Ilie, G., Hagos, B., Heaford, A., Horton, L.,

Rigan, J., Larkocque, K., Lamazares, R., Landers, T., Lehoczky, J.,

McCarthy, M., McEwan, P., McGurk, A., McKernan, K., McPheeters, R.,

McCarthy, M., McEwan, P., McGurk, A., McKernan, K., McPheeters, R.,

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Pisani, C., Pollara, V., Raymond, C., Riley, R., Rogov, P., Rothman, D.,

Pisani, C., Pollara, V., Raymond, C., Riley, R., Popor, P., Rothman, D.,

Yasailev, H., Viel, R., Vo, A., Wilson, B., Wu, X., Wyman, D., Ye, W.J.,

Vassiliev, H., Viel, R., Vo, A., Wilson, B., Wu, X., Wyman, D., Ye, W.J.,

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Young, G., Zainoun, J., Zinmer, A. and Zody, M.

E., Santo, M., Carthy, M., Stojanovic, W., Wilson, B., Wu, X., Wyman, D., Ye, W.J.,

Young, G., Zainoun, J., Zinmer, A. and Zody, M., Caltal, USA

Research, 320 Charles Street, Cambridge, M. 02141, USA

On Mar 25, 2000 this sequence version replaced gi:7210017.

Banthy, M., Sandan, P., McCarthy, RepeatMasker.html

http://ftp.gen
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                                                                                                                                                                                                                                                                                                                                                                                                                  NOTE: This is a 'working draft' sequence. It currently consists of 32 contigs. The true order of the pleces not known and their order in this sequence record is arbitrary Gaps between the contigs are represented as runs of N, but the exact sizes of the gaps are unknown. This record will be updated with the finished sequence as soon as it is available and the accession number will be preserved.
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1389: contig of 1389 bp in length
1489: gap of 100 bp
3130: contig of 1641 bp in length
3230: gap of 100 bp
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GCCCAGCCTGTCGCTGGCTGG 109	Length 168347

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37277: contig of 3463 bp in length
42302: contig of 4925 bp in length
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71568: gap of 100 bp
83112: contig of 694 bp in length
716678: gap of 100 bp
83312: contig of 6641 bp in length
90053: contig of 6641 bp in length
90153: gap of 100 bp
90153: gap of 100 bp
90153: gap of 100 bp

FEATURES source

99427 | 99526; gap of 100 bp 99527 | 108015; contig of 8489 bp in length 98116 | 108115; gap of 100 bp 98116 | 118144; contig of 10029 bp in length 18145 | 13844; gap of 100 bp 18245 | 130468; contig of 12224 bp in length 10469 | 130568; gap of 100 bp 10259 | 142239; contig of 11671 bp in length 12240 | 14239; gap of 100 bp 12240 | 14239; gap of 100 bp 12340 | 157135; contig of 14796 bp in length 157235; gap of 100 bp 157235; gap of 100 bp 157236; lés347; contig of 11112 bp in length 1. 168347; contig of 18796; bp in length

100 bp of 9273 bp in length

misc_feature misc_feature misc_feature

> /note=|"assembly_fragment" |490. |.3130 /clone_"RP11-451H23" /clone_lib="RPCI-11 Human

Male BAC"

"assembly_fragment" .4942

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143807 TGG 143805
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                                                                                                                                                                                                               240;
                                                                                                                                                                                                                                                                                                                                                                                                                              www.jgi.de.gov
www.jgi.de.gov
Finishing Completed at Stanford Human Genome Center
www-shgc.stanford edu
Quality: Phrap Quality >=40 99.8% of Sequence;
Estimated Total Number of Errors is 0.9.
NOTE: Shatter libraries failed to verify the dinucleotide repeat
region 124370-125308. Unsure number of repeat copies
124370-125308. Forced join 124996.
Location/Qualifiers
                                                                                                                                                                                 50
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Direct Submission
Submitted (25-MAY-2002) Production Sequencing Facility, DOE Joint Genome Institute, 2800 Mitchell Drive, Walnut Creek, CA 94598, USA
3 (bases 1 to 190024)
DOE Joint Genome Institute and Stanford Human Genome Center.
Direct Submission
Submitted (04-MAR-2003) DOE Joint Genome Institute, 2800 Mitchell Drive, Walnut Creek, CA 94598, USA
On Mar 4, 2003 this sequence version replaced g1:21206277.
Draft Sequence Produced by DOE Joint Genome Institute
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             DOE
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AC122714
AC122714.2 GI:28827858
                                                                                                                                                                                                                             Similarity
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Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 190024)
DDE Joint Genome Institute and Stanford Human Genome Center.
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                          TGAAGCTCCTGCTGAGCAGCCTGGGCATCCCCGTGAACCACCTCATAGAGGGCTCCCAGA
                                                                                      AGTCGGCGGCGGAGGCCGGGGCCGGGACCCTGGCCAACCCCTCGGCACCCTCAACCCGC
                                                                                                                                                TGG
 AGTGTGTGGCTGAGCTGGGTCCCCAGGCCGTGGGGGCCCTGAAGGCCCTGC
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Joint Genome Institute.
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                                                                                                                                                                                                                                                                                         D)
                                                                                                                                                                                                                                                                                                                                              /organism "Homo sapiens"
/mol_type="genomic DNA"
/db_xref="taxon:9606"
/chromosome="5"
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124370. 125308
                                                                                                                                                                                                                                                                                  /note="NOTE: Shatter libraries failed to verify the dinucleotide repeat region 124370-125308. Unsure number of repeat copies 124370-125308. Forced join 124996." a 46028 c 46121 g 52268 t
                                                                                                                                                                                                                          76.3%;
98.8%;
                                                                                                                                                                                                             0;
                                                                                                                                                                                                           Score 238.2; DB of Pred. No. 1.7e-28 O; Mismatches
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ne 5 clone RP11-451H23,
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REFERENCE
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Consensus quality: 110477 bases at least Q40
Consensus quality: 117221 bases at least Q30
Consensus quality: 120225 bases at least Q20
Estimated insert size: 13100; pulse field gel estimation
Estimated insert size: 136288; sum-of-contigs estimation
Quality coverage: 7.48 in Q20 bases; pulse field gel estimation
Quality coverage: 7.76 in Q20 bases; sum-of-contigs estimation
* NOTE: This is a 'working draft' sequence. It currently
* consists of 13 contigs. The true order of the pieces
* is not known and their order in this sequence record is
* arbitrary. Gaps between the contigs are represented as
* runs of N, but the exact sizes of the gaps are unknown.
* This record will be updated with the finished sequence
* as soon as it is available and the accession number will
* be preserved.
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Center Project Name: 78060
Center Project Name: CIT978SKB_36B8
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo. 1 (bases 1 to 127488)
DOE Joint Genome Institute.
Sequencing of Human Chromosome 5
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              127488 bp DNA linear Homo sapiens chromosome 5 clone CTB-36B8, WORKING 13 unordered pieces.
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DOE Joint Genome Institute.
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PHASE1; HTGS_DRAFT; HTGS_ACTIVEFIN
                                  10237:
10337:
12440:
12540:
15935:
16035:
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1216:
2254:
2354:
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of 3395
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of 1493
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of 8361
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8 bp in length
a length
by in length
by in length
by in length
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a length
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DRAFT SEQUENCE,
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RESULT 15
BD082139
LOCUS
DEFINITION
VERSION
VERSION
KEYWORDS
SOURCE
ORGANISM
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AUTHORS
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JOURNAL
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Best Local Similarity 98.4%;
Matches 240; Conservative
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                                                                                           Zea mays

Zea mays

Zea mays

Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Bukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; PACCAD

Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; PACCAD

Lade; Panicoideae; Andropogoneae; Zea

Ediade; P.N., Gordon, J., Colpitts, T.L., Friedman, P.N., Gordon, J., Redel, P.N., Hodges, S.C., Klass, M.R., Kratochvil, J.D., Rapp, L.R., Russell, J.C. and Stroupe, S.D.

Reagents and methods useful for detecting diseases of the lung

ABBOTT LABORATORIES

PN JP 2001522225-A 3 13-NOV-2001;

ABBOTT LABORATORIES

PN JP 2001522225-A 3 13-NOV-2001;

PI 30-JAN-1998 JP 1998533078

PF 31-JAN-1997 US 08/791710

PI PATRICIA MEDILING MEDEL, MAURICE COHEN, TRACEY L COLPITTS, PAULA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             110 AGTCGGCGGCGGAGGCCGGGGCCGGGACCCTGGCCAACCCCTCGGCACCCTCAACCCGC
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JP 2001522225-A/3.
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JON D KRATOCHVIL, LISA ROBERTS RAPP, JOHN C RUSSELL, STEPHEN D
STROUPE
                                                 JULIAN GORDON, EDWARD N GRANADOS, STEVEN C HODGES, MICHAEL R PI
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1. 127488
/organism="Homo sapiens"
/mol_type="genomic DNA"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       /clone="CTB-36B8"
/clone_lib="CalTech human BAC library B"
32392 c 31616 g 30626 t 1211 others
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   /db_xref="taxon:9606"
/chromosome="5"
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39185: gap of unknown length
60545: contig of 21360 bp in length
79490: contig of 18845 bp in length
79590: gap of unknown length
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Score 227.2; DB 2;
Pred. No. 9.6e-27;
0; Mismatches 3;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          linear PAT 27-AUG-2002 diseases of the lung.
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                                  181 GGC
                310 GGC 312
                                                                      h 58.7%; Score 183; I Similarity 100.0%; Pred. No. 2. 83; Conservative 0; Mismatches
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Strandedness: Single;
C Topology: Linear;
H Key Location/Qualifiers.
                                                                                                                                                                                            /organism="zea mays"
/mol_type="genomic DNA"
/db_xref="taxon:4577"
76 c 74 g
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Location/Qualifiers
1. .225
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2.6e-19;
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Search completed: September 20, 2003, 00:34:59
Job time: 1404.59 secs

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Perfect score:
Sequence:
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Maximum Match 100%
Listing first 45 summaries
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Maximum DB seq length: 2000000000
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                                                                                                                                                                                                                                                                                                                                                                                                                                                     2888711 seqs, 20454813386 residues
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Gapop 10.0 , Gapext 1.0
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em_htg_hum:*
em_htg_inv:*
em_htg_other:*
em_htg_other:*
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em_pat: *
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Pred. No.

is

the number of results predicted by chance to have a

score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

RESULT 1 AC022095/c LOCUS DEFINITION ACCESSION VERSION KETWORDS SOURCE ORGANISM REFERENCE AUTHORS TITLE			C 37	C C 33	0 0 0 0 0 3 2 9 3 2 1 0		c 2211		c c 112 154	98765	4321	Result
2 4 17	58. 6	, , , , , , , , , , , , , , , , , , ,	58.88	യ യ	00111	ط سر سر د	PPB0	64.66			88. 48 48	Score
ACO22095 HOMO sapiens c HOMO sapiens c ACO22095 ACO22095 HTG: HTGS: PHAS HOMO sapiens Eukaryota; Met Mammalia; Euth L (base 1 tc DOE Joint Gen Sequencing of		10.666								21.8 21.8 21.2 14.2	88.7 88.2 88.2 86.9	Query Match
PH ed										166777 562 190 519 569	127488 127488 168347 190024 130129	Length
chromosome pieces. gi:1369618 ASE1; HTGS_[(human) etazoa; Chor ttberia; Prin to 127488) nome Institt	φ.	, waaaa	200	11 9 11	0000	9210	2212	2 11 2	129666	, യ യ യ യ ഗ ।	2000	DB
5 clone 5 clone RAFT; H7 rdata; C1 nates; C2 ite.		AX33281 AX33304 AX41130 AX41130		PM2B12B AC011407 PM7G11B	ACC112672 ACC112672 ACC141419 ACC141419	AF411253 AC139773 AF429315	AC022663 PM2H12B AC027353 AC141871	AC084804 AC022663 PM12H12B PM3H11G	AK403520 AX403520 BD082138 AF429315 AP005772 PM2H12G	AC106813 BD082141 BD082137 BD082142 BD082142 AX201348	AC022095 AC025336 AC025314 AC122714 AC108083	ID
DNA TB-36B8, S_ACTIVE niata; V	rs											
near RKING DR ebrata; minidae;	AE00646	AX33281 AX333304 AX41130 Z84721	AC06661 AC13810	AL6846 AC01140 AL6851	AC09109 AC11267 AC141411 AP00574	AF41129 AC13977; AF42931;	AC02266 AL6848 AC02735 AC14187	AC084804 AC022663 AL68449 AL68574	AX40350 BD082138 BF429315 AF429315 AP005777	AC106813 Ho BD082141 Ro BD082137 Ro BD082142 Ro BD082142 Ro AR201348 So	AC022095 AC025336 AC122714 AC108083	Descript
HTG 20-APR-2001 AFT SEQUENCE, Euteleostomi;	2 Homo sap1	equequequequequequequequequequequequeque	0 Homo sapi 9 Mus muscu	95 Penicilli 7 Homo sapi 96 Penicilli 71 penicilli	Papio anu 2 Mus muscu 9 Pan trogl 3 Oryza sat	3 Mus muscu 3 Homo sapi 5 Homo sapi	omo sapi Penicill omo sapi us muscu	Homo sapi 55 Penicilli 19 Penicilli	sequence sequence Reagents Homo sapi Oryza sat O Penicilli	omo eage eage eage	Homo sapi Homo sapi Homo sapi Homo sapi	ion

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REFERENCE
AUTHORS
TITLE
                                                                                                                                                                                BASE COUNT
ORIGIN
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                                                          Query Match
Best Local Similarity 95.8%;
Matches 529; Conservative
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Consensus quality: 110477 bases at least Q40

Consensus quality: 117221 bases at least Q30

Consensus quality: 120225 bases at least Q20

Estimated insert size: 131000; pulse field gel estimation

Estimated insert size: 136288; sum-of-contigs estimation

Quality coverage: 7.48 in Q20 bases; pulse field gel estimation

Quality coverage: 7.76 in Q20 bases; pulse field gel estimation

Quality coverage: 7.76 in Q20 bases; pulse field gel estimation

Quality coverage: 7.76 in Q20 bases; pulse field gel estimation

* NOTE: This is a 'working draft' sequence. It currently

* consists of 13 contigs. The true order of the pieces

* is not known and their order in this sequence record is

* arbitrary (ags between the contigs are represented as

* runs of N, but the exact sizes of the gaps are unknown.

* This record, will be updated with the finished sequence

* as soon as it is available and the accession number will

* be preserved.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Submitted (26-JAN 2000) Production Sequencing Facility, DOE Joint Genome Institute, 2800 Mitchell Drive, Walnut Creek, CA 94598, USA On Apr 20, 2001 this sequence version replaced gi:7711676.

------Genome Center Center: Joint Genome Institute Center: Joint Genome Institute Center Code: UGI
1 CGGCCGGGGAGGCCGGGAGTGAGGCCTGATCGTCCCTGGCGCCTCCACCTCCCAGG 60
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Center Project Name: 78060
Center clone name: CIT978SKB_36B8
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2 (bases 1 to 127488)

DOE Joint Genome Institute.

Direct Submission
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10338
125441
125441
15936
16036
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24497
239086
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60546
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5005: contig of 1493 bp in length
5105: gap of unknown length
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Pred. No. 1.4e-72;
0; Mismatches 5;
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                                                                                                                     Length 127488;
                                                          2;
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RESULT 2 AC025336/c LOCUS DEFINITION ACCESSION VERSION KEYWORDS SOURCE ORGANISM REFERENCE AUTHORS TITLE JOURNAL REFERENCE AUTHORS	Ωy Db 83	Qy Db 83	Ωy 83	Фу 83	ОУ Db 84	Qy Db 84	Qy Db 84	Ωy Db 84	Оу	Db 84
ACO25336 ACO2536 ACO25	540 AGCCCCCGCGCC 551 768 AGCCCCGCGCC 83757	480 ACCGGGTATAAGAAGCCTCGTGGCCTTGCCCGGGCAGCCGCAGGTTCCCCGCGCGCG	420 GAGCGGAGCGGCAGGGCTTTCTCAGGAGCGCGGGGGGGGG	360 GGGCACGGCCTTCCCAGGGCCCGCCGCCGCAGCAGGAGCTTGGCCAGGGCACGGCCGT 419	301 CT-CTCTCAGAGGGCCCCAGCGCCTGCCAAGAGGAAGTCCTCGAGGCCCCGGGCAGGGAAG 359 	241 AGACCGCAAAGCGAAGGTGCGGGCCGGGGTGGGCCTCGCGGAGACAAAGGCCGGGCCTGC 300	181 CCCTCACCNGAGGGAAGCTCCCCTCACCCGGCCCAGCCCTGCAGGGGGGGG	121 CAGGGACCAGGGAGCCAGGAACTGCGCCCGCCCCCCCCCC	61 CGCAGAAGGCGCCCACGAGGACCCCCAGTGCCCGACGTTGCCACGGTCTGGGATCAGAGG 120	

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COMMENT
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Direct Submission
Submitted (08-MAR-2000) Whitehead Institute/MIT Center for Genome Submitted (08-MAR-2000)
Research, 30 Charles Street, Cambridge, MA 02141, USA 00 MAR-25, 2000 this sequence version replaced gi:7210017.
All repeats were identified using RepeatMasker:
Smit, A. F. A. & Green, P. (1996-1997)
http://ftp.genome.washington.edu/RW/RepeatMasker.html
http://ftp.genome.washington.edu/RW/RepeatMasker.html
http://ftp.genome.washington.edu/RW/RepeatMasker.html
http://ftp.genome.washington.edu/RW/RepeatMasker.html
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http://ftp.genome.wi.mit.edu
Center code: WIBR
Web site: http://www-seq.wi.mit.edu
Contact: sequence_submissions@genome.wi.mit.edu
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Consensus quality: 15924 bases at least Q20 consensus quality: 15924 bases at least Q20 consensus quality: 150313 bases; sum-of-contigs Quality coverage: 3.6 in Q20 bases; sum-of-contigs
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                NOTE: This is a 'working draft' sequence. It currently consists of 32 contigs. The true order of the pieces is not known and their order in this sequence record is arbitrary. Gaps between the contigs are represented as runs of N, but the exact sizes of the gaps are unknown. This record will be updated with the finished sequence as soon as it is available and the accession number will be preserved.
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10387
12313
12313
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       sapiens
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Pred. No. 3.6e-72;
0; Mismatches 5;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Length 168347;
               linear
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inear PRI 04-MAR-2003 complete sequence.
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AUTHORS
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VERSION
KEYWORDS
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AUTHORS
TITLE
JOURNAL
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Best Local Sim
Matches 528;
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AL Submitted (04-MAR-2003) DOE Joint Genome Institute, 2800 Mitchell Drive, Walnut Creek, CA 94598, USA On Mar 4, 2003 this sequence version replaced gi:21206277. Draft Sequence Produced by DOE Joint Genome Institute Finishing Completed at Stanford Human Genome Center www-shgc.stanford.edu Quality: Phrap Quality >=40 99.8% of Sequence; Shatter libraries failed to verify the dinucleotide repeat region 124370-125308. Unsure number of repeat copies Location/Qualifiers

1 190024
                                                                                                                                                               81351
                                                                                                                                                                                                          81291
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                                                                                     241
                                                                                                                                       181
                                                                                                                                                                                          121
                                                                                                                                                                                                                                                                            1 CGGCCGGGAGGCGGCCGGGAGTGAGGCCTGATCGTCCCTGGCGCCTCCACCTCCCCAGG 60
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                                                                                                                                                       CAGGGACCAGGGAGCCAGGAACTGCGCCGCCCCGCCCCTGCCCTGGCGCGAGGGAAGCT
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AC122714.2
HTG.
                                                                                                      2 (bases 1 to 190024)
DOE Joint Genome Institute.
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DOE Joint Genome Institute and Stanford Human Genome Center.
                                                   AGACCGCAAAGCGAAGGTGCGGGCCGGGGTGGGCCTCGCGGAGACAAAGGCCGGGCCTGC
                                                                     AGACCGCAAAGCGAAGGTGCGGGCCGGGGTGGGCCTCGCGGAGACAAAGGCCGGGCCTGC
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                                                                                                                                                                                                                                                                                                                   Conservative
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                                                                                                                                                                                                                                                                                                                                                                         /note="NOTE: Shatter libraries failed to verify the dinucleotide repeat region 124370-125308. Unsure number of repeat copies 124370-13308. Forced join 124996." a 46028 c 46121 g 52268 t
                                                                                                                                                                                                                                                                                                                                                                                                                                 /clone="RP11-451H23"
124370. .125308
                                                                                                                                                                                                                                                                                                                                                                                                                                                         /organism="Homo sapiens"
/mol_type="genomic DNA"
/db_xref="taxon:9606"
/chromosome="5"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          GI:28827858
                                                                                                                                                                                                                                                                                                                            88.2%;
95.7%;
                                                                                                                                                                                                                                                                                                               Score 486; DB 9; I
Pred. No. 3.4e-72;
0; Mismatches 5;
                                                                                                                                                                                                                                                                                                                                        Length 190024;
                                                                                                                                                                                                                                                                                                                Indels
                                                                                                                                                                                                                                                                                                               19;
                                                                                                                                                                                                                                                                                                               Gaps
                            359
                                                                                                                                 240
                                                                                                                                                                                                                                    120
   81130
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Query Match Best Local

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RESULT 3
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AC122714 Homo sapi

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RESULT 4 AC108083/c LOCUS

DEFINITION

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ACCESSION VERSION KEYWORDS SOURCE ORGANISM

REFERENCE AUTHORS TITLE JOURNAL REFERENCE AUTHORS TITLE JOURNAL

COMMENT

FEATURES Source

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Consensus quality: 124488 bases at least Q40
Consensus quality: 128031 bases at least Q30
Consensus quality: 128042 bases at least Q30
Consensus quality: 128842 bases at least Q30
Consensus quality: 128842 bases at least Q30
Estimated insert size: 135000; agarose-fp estimation
Quality coverage: 7.66 in Q20 bases; sum-of-contigs estimation
Quality coverage: 7.97 in Q20 bases; sum-of-contigs estimation.

* NOTE: This is a 'vorking draft' sequence. It currently

* consists of 4 contigs. The true order of the pieces

* is not known and their order in this sequence record is

* arbitrary. Gaps between the contigs are represented as

* arbitrary. Gaps between the contigs are represented as

* runs of N, but the exact sizes of the gaps are unknown.

* This record will be updated with the finished sequence

* as soon as it is available and the accession number will

* be preserved......
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Homo sapiens chromosome 5 clone CTD-2013L15, SEQUENCE, 4 unordered pieces. AC108083
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Homo sapiens
Eukaryota; Metazoa; Chordata; (
Eukaryota; Metheria; Primates; (
Mammalla; Eutheria; Primates; (
1 (bases 1 to 130129)
DOE Joint Genome Institute.
Sequencing of Human Chromosome
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Direct Submission
Direct Submission
Sequencing Submitted (25-JAN-2002) Production Sequencing Submitted (15-JAN-2002) Production Sequencing Submitted (15-JAN-200
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               AC108083
AC108083.1 GI:18369929
HTG; HTGS_PHASE1; HTGS_
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Genome Institute, 2800 Mitchell
------Genome Center Institute
Center: Joint Genome Institute
Center Code: JGI
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Project Information
Center Project Name: 632820
Center clone name: CITB-H1_2013L15
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ACCGGGTATAAGAAGCCTCGTGGCCTTGCCCGGGCAGCCGCAGGTTCCCCGCGCGCCCCG 539
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g Joint Genome Institute.
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sapiens
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4421
23713
23813
23813
48603
48703
/organism="Homo
                                              location.
                                      4320: contig of 4320 bp in length
4420: gap of unknown length
23712: contig of 19292 bp in length
23812: gap of unknown length
48602: contig of 24790 bp in length
48702: gap of unknown length
130129: contig of 81427 bp in length
cation/qualifiers
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     sapiens"
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5, WORKING DRAFT
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Creek, CA
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94598, USA
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Best Local Similarity
Matches 522; Conserv
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Homo sapiens chromosome 5 clone 3 ordered pieces.
AC106813
AC106813.3 GI:19224876
HTGS_PHASE2; HTGS_DRAFT; HT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           CGCAGAAGGCGCCCACGAGGACCCCCAGTGCCCGACGTTGCCACGGTCTGGGATCAGAGGCGCCAGAAGGCGCCCACGAGGTCAGAGGCGCCCAGAGGACGTTGCCACGGTCTGGGATCAGAGGCGCAGAAGGCGCCCACGAGAGGAGCCCCAGTGCCCACGTTGCCACGGTCTGGGATCAGAGG
                                                                                                                                 Eukaryota; Metazoa; Chordata; (
Mammalia; Eutheria; Primates; (
Mames 1 to 166777)
DOE Joint Genome Institute.
Sequencing of Human Chromosome
                                                                                                                                                                                                                                                     Homo sapiens (human)
Homo sapiens
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                                                                  Unpublished
2 (bases 1 to 166777)
DOE Joint Genome Institute.
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/clone="iD="CalTech human B
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Pred. No. 6.
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                                                                                                                                                                                                                                                                                                          HTGS_ACTIVEFIN
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RP11-586L9, WORKING
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t 300 others
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                              Sequencing
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                              Facility,
                                                                                                                                                                                                                       Euteleostomi;
Homo.
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DRAFT SEQUENCE,
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                                   DOE Joint
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24390 180 120 24510 60

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Source
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AUTHORS
TITLE
                                                                                                                                                                                                                                                                                                                                                                                                                         Query Match
Best Local
                                                                                                                                                                                                                                                                                                                                                                                                    Best Local Similarity Matches 528; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           JOURNAL
                                                                                                                                                                                                                                               61 CGCAGAAGGCGCCCACGAGGACCCCCAGTGCCCGACGTTGCCACGGTCTGGGATCAGAGG 120
                                                                                                                                                                                                                                                                                                                        1 CGGCCGGGGAGGCGGCGGGAGTGAGGCCTGATCGTCCCTGGCGCCTCCCACCTCCCCAGG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Consensus quality: 163497 bases at least Q40
Consensus quality: 166432 bases at least Q30
Estimated insert size: 186550; agarose-fp estimation
Quality coverage: 9.4 in Q20 bases; sum-of-contigs estimation
Quality coverage: 10.51 in Q20 bases; sum-of-contigs estimation

**NOTE: This, is a 'working draft' sequence. It currently
consists of 3 contigs. Gaps between the contigs
**are represented as runs of N. The order of the pieces
**is believed to be correct as given, however the sizes
**of the gaps between them are based on estimates that have
**provided by the submittor.

**This sequence will be replaced
**the accession number will be preserved.

**the accession number will be preserved.

**C238 | 62337: contig of 62237 bp in length
** 6238 | 75937: gap of unknown length
** 75938 | 156777: contig of 90840 bp in length
** 75938 | 166777: contig of 90840 bp in length.
**Consiston/Oualiflers
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Center Project Name: 1519801
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      -----Genome Center
Center: Joint Genome Institute
Center Code: JGI
Web site: http://www.jgi.doe.gov
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Submitted (07-MAR-2002) Production Sequencing Facility, DOE Joint Genome Institute, 2800 Mitchell Drive, Walnut Creek, CA 94598, USA On Mar 7, 2002 this sequence version replaced gi:18369924.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Summary Statistics
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Center clone name: RPCI-11_586L9
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DOE Joint Genome Institute.
                           AGACCGCAAAGCGAAGGTGCGGGCCGGGGTGGGCCTCGCGGAGACAAAGGCCGGGCCTGC
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       /clone="RP11-586L9"
/clone_lib="RPCI human BAC library
39804 c 41258 g 40888 t 200
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  /db_xref="taxon:9606"
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/organism="Homo sapiens"
/mol_type="genomic DNA"
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95.5%;
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166777)
                                                                                                                                                                                                                                                                                                                                                                                              Score 475; DB 2; I
Pred. No. 2.4e-70;
0; Mismatches 5;
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JP 2001522225~A/5.
Zea mays
                                                                                                                                                      Similarity
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Reagents and methods useful for detecting diseases of the lung.
BD082141
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                                                                                                                                   Conservative
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Key
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31-JAN-1997 US 08/791710
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                                                                                                                                                                                                                      /organism="Zea mays"
/mol_type="genomic DNA"
/db_xref="taxon:4577"
200 c 192 g
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                                                                                                                                                    21.8%;
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Pred. No. 1.4e-10;
0; Mismatches 1
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Gordon, J. Rapp, L.R.,

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RESULT 7
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Best Local Similarity 96.7
Matches 117; Conservative
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RE Medel, P. A. B., Cohen, M., Colpitts, T. L., Friedman, P. N., Gordon, J., Rosses 1. A. Hodges, S. C., Klass, M.R., Kratochvil, J.D., Rapp, L.R., Russell, J.C. and Stroupe, S. D. Reagents and methods useful for detecting diseases of the lung Patent: JP 200152225-A 1 13-NOV-2001; ABBOTT LABORATORIES PN JP 200152225-A/1 198533078 PN JP 30-JAN-1998 JP 198533078 PR 31-JAN-1997 US 08/791710 PT PATRICIA A BILLING MEDEL, MAURICE COHEN, TRACEY L COLPITTS, PAULA PI PATRICIA A BILLING MEDEL, MAURICE COHEN, TRACEY L COLPITTS, PAULA
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Reagents and methods useful f
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JP 2001522225-A/1.
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BD082142 519
Reagents and methods useful
BD082142
BD082142.1 GI:22627752
JP 2001522225-A/6.
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C Topology: Linear;
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C12N15/63, C12N5/10, C12Q1/68, C07K14/47//C07K16/30, G01N33/574 CC
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/mol_type="genomic DNA"
/db_xref="taxon:4577"
69 c 67 g
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ISM Zea mays

Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;

Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;

Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; PACCAD

Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; PACCAD

Clade; Panicoideae; Andropogoneae; Zea.

Clade; Panicoideae; PacCAD

Ressell, J. Cohen, M., Colpitts, T.L., Friedman, P.N., Gordon, J.,

Rassell, J.C., Hodges, S.C., Klass, M.R., Kratochvil, J.D., Rapp, L.R.,

Russell, J.C., Hodges, S.C., Klass, M.R., Kratochvil, J.D., Rapp, L.R.,

Russell, J.C., Hodges, S.C., Klass, M.R., Kratochvil, J.D., Rapp, L.R.,

Russell, J.C., and Stroupe, S.D.

Russell, J.C., and Stroupe, S.D.

Rasgents and methods useful for detecting diseases of the lung

Patent: JP 200152225-A 6 13-NOV-2001;

ABBOTT LABORATORIES

PN JP 2001522225-A 6 13-NOV-2001;

PD 13-NOV-2001

PD 1
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1 Similarity 100.0%; Pred. No. 0.0014;
78; Conservative 0; Mismatches 0;
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Sequence 27 from Patent WO0153486.
AX201348 .1 GI:15391167
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PI
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                                                                                                                                                                                                                                                                                                                                               Homo sapiens (human)
                                                                                                                                                            Genentech,
                                                                                                                                                                                                                                                                                                        Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
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Strandedness: Single:
C Topology: Linear;
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/mol_type="genomic DNA"
/db_xref="taxon:4577"
190 c 170 g
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                                    /organism="Homo sapiens"
/mol_type="genomic DNA"
/db_xref="taxon:9606"
190 c 170 g 8
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1. .569
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Smith, V.,

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AR252648
LOCUS
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FEATURES
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ORGANISM
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                                                                                                                                     JOURNAL
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Best Local S
Matches 78
                                                                                                                                                                                      TITLE
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Best Local Similarity
Matches 78; Conserv
                                                                 source
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Unclassified.
Unclassified.
1 (bases 1 to 570)
1 (bases 1 to 570)
2 (bases 1 to 570)
2 (bases 1 to 570)
3 (bases 1 to 570)
4 (bases 1 to 570)
4 (bases 1 to 570)
5 (bases 1 to 570)
5 (bases 1 to 570)
6 (bases 1 to 570)
6 (bases 1 to 570)
7 (bases 1 to 570)
7 (bases 1 to 570)
8 (bases 1 to 570)
8 (bases 1 to 570)
9 (bases 1 to 570)
9 (bases 1 to 570)
1 (bases 1 to 
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Genentech Inc. (US)
Location/Qualifiers
                                                                                                                                                                                                 Ashkenazi, A.J., Baker, K.P., Botstein, D., Desnoyers, L., Eaton, D., Ferrara, N., Gerber, H., Gerritsen, M., Goddard, A., Godowski, P., Grimaldi, C.J., [Gurney, A.L., Kijavin, I., Napier, M.A., Pan, J., Paoni, N.F., Roy, M., Stewart, T.A., Tumas, D., Watanabe, C.K., Williams, P., Wood, W.I. and Zhang, Z.
                                                                                                                                                                     Secreted and transmembrane polypeptides and nucleic acids encoding
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      AX403520 Sequence 407 from Patent AX403520
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78; Conservative
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Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
                                                                                                                                                                                                                                                                                                                                                                                                   Homo sapiens (human)
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Sequence 407
AR252648
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11arity | 100.0%; Pred. No. 0.0014;
Conservative 0; Mismatches 0;
        /organism="Homo sapiens"
/mol_type="genomic DNA"
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100.0%; Pred. No.
Live 0; Mismatc
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WO0073454.
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US 6478825.
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RESULT 13
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ORIGIN
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BD082138
LOCUS
DEFINITION
ACCESSION
VERSION
KEYWORDS
SOURCE
ORGANISM
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AUTHORS
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Best Local S
Matches 77
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Б δÃ В δÃ

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Query Match
Best Local
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KS Medel, P.A.B., Cohen, M., Colpitts, T.L., Friedman, P.N., Gordon, J., Granados, E.N., Hodges, S.C., Klass, M.R., Kratochvil, J.D., Rapp, L.R., Russell, J.C. and Stroupe, S.D.

Reagents and methods useful for detecting diseases of the lung ABBOTT LABORATORIES
PN JP 200152225-A 2 13-NOV-2001;
PD 13-NOV-2001
PF 31-JAN-1997 US 08/791710
PI PATRICIA A BILLING MEDEL, MAURICE COHEN, TRACEY L COLPITTS, PAULA
                                                534 GCCCCGAGCCCCCGCGCC 551
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|||||||||||||||||||||||||||||||61 GCCCCGAGCCCCCGCGCC 78
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CC Topology: 1
FH Key
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BD082138 GI:22627748
JP 2001522225-A/2.
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1 Similarity 100.0%;
78; Conservative
GCCCGAGCCCCCGCGCC
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                                                                                                               Conservative
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Key
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                                                                                                                                                                                                                                                                                                                               JON D KRATOCHVIL, LISA ROBERTS RAPP, JOHN C RUSSELL, STEPHEN D
                                                                                                                                                                                                                                                                                                                                                                                       N FRIEDMAN,
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                                                                                                                                                                                       ۵
                                                                                                                                                                                /organism="Zea mays"
/mol_type="genomic DNA"
/db_xref="taxon:4577"
97 c 82 g
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a 190 c 170 g
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98.7%;
 78
                                                                                                             Score 77; DB
Pred. No. 0.00
0; Mismatches
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0.0026;
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TITLE
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Query Match 13.4%; Score 74; DB Best Local Similarity 13.2%; Pred. No. 0.00 Matches 64; Conservative 224; Mismatches
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1 (bases 1 to 125020)

Holmes, S.E., O'Hearn, E., Rosenblatt, A., Callahan, C., Hwang, H.S., Ingersoil-Ashworth, R.G., Fleisher, A., Stevanin, G., Brice, A., Potter, N.T., Ross, C.A. and Margolls, R.L.

A repeat expansion in the gene encoding junctophilin-3 is associated with Huntington disease-like 2 associated with Huntington disease-like 2
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Homo sapiens junctophilin 3
AF429315
AF429315.1 GI:17646244
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Holmes, S.E., Ingersoll-Ashworth, R.G., Ross, C.A. and Margo
Holmes, S.E., Ingersoll-Ashworth, R.G., Ross, C.A. and Margo
Direct Submission
Submitted (05-0CT-2001) Psychiatry, Johns Hopkins Medical
Submitted (05-0CT-2001) Psychiatry, Johns Hopkins Medical
Institutions, 600 N. Wolfe St., Baltimore, MD 21287, USA
Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Homo sapiens
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                                                                                                                                                                                             KSYRRKRSYYYWGGGKRAKKKYYCAGRRRRMSYWKCCAKWWMSYCCWSYCMTYYYSKSCT 17575
                                                                                                                                                                                                                                                        YKSSTCYKRGGYYWGSKTCYSAGGKSRSMYYCMMRSSKSSSWSMSMARSSWCMGWGAGYR 17515
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GGGGGCGCGTGGGGTCAGACCGCAAAGCGAAAGGTGCGGGCCGGGGTGGGCCTCGCGGAGA 284
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/note="isolated from a patient with Huntington's
Disease-Like 2 (HDL2)"
complement(35581. .35746)
/rpt_type=tandem
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   /Product="junctophilin 3"
/product="junctophilin 3"
/product="junctophilin 3"
/protein_id="AAL40941.1"
/protein_id="AAL40941.1"
/protein_id="AAL40941.1"
/protein_id="AAL40941.1"
/protein_id="AAL40941.1"
/product="Junctophilin"
/product="Junctophi
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/gene="JPH3"
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/mol_type="genomic DNA"
/db_xref="taxon:9606"
/chromosome="16"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             /product="junctophilin 3" complement(<36507. .36887)
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complement(<36507. .>36887)
/gene="JPH3"
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membrane and endoplasmic reticulum"
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HTGS_PHASE2.
OTYZA SATIVA (Japonica cultivar-group)
OTYZA SATIVA (Japonica cultivar-group)
OTYZA SATIVA (Japonica cultivar-group)
Eukaryota; Viridiplantae; Streptophyta; En
Spermatophyta; Magnoliophyta; Liliopsida;
Ehrhartoideae; OTYZeae; OTYZa.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   AP005772 172650 bp DNA oryza sativa (japonica cultivar-group) choosunaa0073A21, *** SEQUENCING IN PROGRESS
                                                                                                                                                                                                                                                                    NOTE: It currently consists of I contigs. Gaps between the contigs are represented as runs of N. The order of the pieces is believed to be correct as given, however the sizes of the gaps between them are based on estimates that have provided by the submitter. This sequence will be replaced by the finished sequence as soon as it is available and the accession number will be preserved.

* NOTE: This is a 'working draft' sequence.

* This sequence will be replaced

* by the finished sequence as soon as it is available and

* the accession number will be preserved.

Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Submitted (25-SEP-2002) Takuji Sasaki, National Institute of Submitted (25-SEP-2002) Takuji Sasaki, National Institute of Agrobiological Sciences, Rice Genome Research Program; Kannondai Agrobiological Sciences, Rice Genome Research Program; Kannondai Agrobiological Sciences, Japan (25-Sept.) Tsukuba, Tbaraki 305-8002, Japan (E-mail:tsasaki@inlas.affrc.go.jp, URL:http://rgp.dna.affrc.go.jp/, Tel:81-298-38-7441, Fax:81-298-38-7468)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Published Only in Database (2002) 2 (bases 1 to 172650) Sasaki, T., Matsumoto, T. and Katay
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Sasaki,T., Matsumoto,T. and Katayose,Y Oryza sativa nipponbare(GA3) genomic Diclone:OSJNBa0073A21
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                                                                                                                                  /organism="Oryza sativa (
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/cultivar="Nipponbare"
/db_xref="taxon:39947"
/chromosome="2"
                                                                                      /clone="OSJNBa0073A21"
34714 c 35062 g 49
  12.9%;
     Score 71; DB 2;
Pred. No. 0.0037;
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Query Match 12.4%; Score 68.2; DB 11; Length 1279; Best Local Similarity 45.3%; Pred. No. 0.046; Matches 231; Conservative 0; Mismatches 273; Indels 6; Gaps 2;	DATH12G/C DATH12G DEFINITION DEFINITION ALGB4840 ACCESSION ALGB4840 VERSION ALGB4840.1 GI:19337636 SOURCE ORGANISM REFERENCE AUTHORS TITLE JOURNAL AUTHORS AUTHORS AUTHORS TITILE JOURNAL AUTHORS DATHORS TITLE JOURNAL LOCALIJO JOURNAL JOURNAL JOURNAL JOURNAL JOURNAL LOCALIJO JOURNAL JOUR	Db 91122 CGGGGCCCCNCCCGGGGGCGGGGGGGGGGCCNNGCCGGCCGC 91080 RESULT 15		pb 91182 cccagaaccaaccaaccaaccaaccaaccaaccaaccaa	448	Oy 388 CCGCAGCAGGAAGTTGGCCAGGGCACGCGCGTGAGCGGAGGGGGGGG	Db 91302 GCGGCCCCGGGGGCGCCCGCGCGCCCCGCGGGCCCCCCGCC 91243	Qy 334 AAGTCCTCGAGGCCCGGGCAGGGAAGGGGGCACGGGCTTCCCAGGGCCCGGCGG 387	274 CCTCGCGGAGACAAAGGCCGGGCCTGCCTCTCTCAGAGGGCCCCAGCGCCTGCCAAGAGGG	91422 GNNGGCGGGGCCCGCGGGGGGGGGGGGGGGGGGGGGG	Db 91482 CCGGCCCGGGCGGCGCGCGCGGCGGGGGGCCGGGGGGCCGGCGNCNCCCCCC	154 CGCCCTGCCCTGGCGCGAGGGAAGCTCCCTCACCNGAGGGAAGCTCCCCTCACCGGCC	91542 NNNNNNNNNGGGCCGCGGCGCGCGCGCGCGCGCGCGCGC	Db 91602 CGCACCTACCGGCGCAAACTGNNNNNNNNNNNNNNNNNNN	34 CGTCCCTGGCGCCTCCACCTCCCCAGGCGCAGAAGGCGCCCACGAGGAGCCCCCAGTGCCC	Matches 222; Conservative 0; Mismatches 295; Indels 6; Gaps 1;
•		Search completed: September 20, 2003, 00:35:05 Job time: 2472.41 secs	Db 762 GCGCGGGCCCGGCCGGCCCGGCCCGGCCGC 733	Qy 521 AGGTTCCCCGCGCGCGCGCGAGCCCCCGCGC 550	822	Db 877 NCCCCNCGCGTGCGGCGCGCGGCCGCGCGCGCGCGCGCGCGCGCG	TIGGCCAGGGCACGCCGTGAGCCGAGCCGAGGCTTTCTCAGGAGCGCGAGGC	Db 937 CGGGGCCGNNGGGCGGCCGNNCGGGCCGCCGGCCGGCCG	997	281	OY 222 CARGEGEGEGEGEGEGEGEGEGEGEGEGEGGGGGGGGGGG	1117	162 CCTGGCGCGAGGGAAGCTCCCTCACCNGAGGGAAGCTCCCCTCACCCGGCCCAGCCCTG	OY 102 CACGGTCTGGATCAGAGCAGGACCAGGACCAGGAGCGCGCGC	1237 GCGCCNCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCC	Qy 42 GCGCCTCCACCTCCCCAGGCGCAGAAAGGCGCCCAAGGACCCCCAGTGCCCGACTTGC 101

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Scoring table: Sequence: Title: Perfect score:

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Total number of hits satisfying chosen parameters:
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score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.
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1: /cgn2_6/ptodata/2/lna/5A_COMB.seq:*

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5: /cgn2_6/ptodata/2/lna/BCTUS_COMB.seq:*

6: /cgn2_6/ptodata/2/lna/backfiles1.seq:*
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4 US-09-96-243-407
5 PCT-US91-06532-1
5 PCT-US91-06532-1
3 US-09-103-040A-1
1 US-08-223-463-14
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                   APPLICANT: PAON', James
APPLICANT: Ray, Margaret Ann
APPLICANT: Stewart, Timothy A.
APPLICANT: Stewart, Timothy A.
APPLICANT: Stewart, Timothy A.
APPLICANT: Williams, Daniel
APPLICANT: Williams, D. Mickey
APPLICANT: Williams, D. Mickey
APPLICANT: Williams, D. Mickey
APPLICANT: Williams, D. Mickey
APPLICANT: Zhang, Zemin
APPLICANT: Zhang, Zemin
TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
TITLE OF INVENTION: Acids Encoding the Same
FILLE APPLICATION NUMBER: 60/049787
PRIOR APPLICATION NUMBER: 60/049787
PRIOR FILLING DATE: 1997-06-16
PRIOR FILLING DATE: 1997-06-16
PRIOR APPLICATION NUMBER: 60/062250
PRIOR APPLICATION NUMBER: 60/065311
PRIOR APPLICATION NUMBER: 60/065311
PRIOR APPLICATION NUMBER: 60/065311
PRIOR APPLICATION NUMBER: 60/065311
PRIOR APPLICATION NUMBER: 60/06570
PRIOR APPLICATION NUMBER: 60/06570
PRIOR APPLICATION NUMBER: 60/06570
PRIOR APPLICATION NUMBER: 60/075945
PRIOR APPLICATION NUMBER: 60/075945
PRIOR FILLING DATE: 1998-02-25
PRIOR APPLICATION NUMBER: 60/078910
PRIOR APPLICATION NUMBER: 60/078910
PRIOR APPLICATION NUMBER: 60/083322
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APPLICANT: Baker, Kevin P.
APPLICANT: Bustein, David
APPLICANT: Bustein, David
APPLICANT: Bustein, David
APPLICANT: Besnoyers Luc
APPLICANT: Besnoyers Luc
APPLICANT: Gesnoyers, Luc
APPLICANT: Gerber, Hanspeter
APPLICANT: Gerber, Hanspeter
APPLICANT: Gerber, Hanspeter
APPLICANT: Gerber, Mary E.
APPLICANT: Godowski, Paul J.
APPLICANT: Gunney, Austin L.
APPLICANT: Kljavin, Ivar J.
APPLICANT: Napier, Mary A.
APPLICANT: APPL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           sequence 407, Application US/09996243 patent No. 6478825 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                43.88
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Grinaldi, J. Christopher
Grinaldi, J. Christopher
Gurney, Austin L.
Kijavin, Ivar J.
Napier, Mary A.
Pan, James .
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Gerritsen, Mary E.
Goddard, Audrey
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US-09-252-991A-5540

US-09-256-691B-14

US-09-209-668-10

US-09-256-952-8

US-08-755-420-1

US-08-658-136-2

US-08-658-136-2

US-08-658-136-1

US-08-68-333-36

US-09-833-371A-36

US-09-833-471A-36

US-09-679-298A-1

US-09-679-298A-1

US-08-770-379-17

US-08-770-379-17

US-08-770-379-17

US-08-770-379-17

US-08-770-379-17

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Sequence 6540, Ap
Sequence 10, Appl
Sequence 10, Appl
Sequence 1, Appl
Sequence 36, Appl
Sequence 36, Appl
Sequence 11, Appl
Sequence 17, Appl
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		9653 907 907 908 947 948 952 946 252 246 252 246 252 254 131 135

PRIOR APPLICATION NUMBER: 60/084600
PRIOR FILING DATE: 1998-05-07
PRIOR FILING DATE: 1998-06-02
PRIOR FILING DATE: 1998-06-02
PRIOR FILING DATE: 1998-06-02
PRIOR FILING DATE: 1998-06-02
PRIOR APPLICATION NUMBER: 60/08769
PRIOR APPLICATION NUMBER: 60/08025
PRIOR APPLICATION NUMBER: 60/08025
PRIOR APPLICATION NUMBER: 60/08026
PRIOR PILING DATE: 1998-06-04
PRIOR APPLICATION NUMBER: 60/08028
PRIOR FILING DATE: 1998-06-04
PRIOR PRIOR APPLICATION NUMBER: 60/08029
PRIOR FILING DATE: 1998-06-04
PRIOR APPLICATION NUMBER: 60/08029
PRIOR FILING DATE: 1998-06-04
PRIOR APPLICATION NUMBER: 60/08023
PRIOR FILING DATE: 1998-06-04
PRIOR APPLICATION NUMBER: 60/08023
PRIOR FILING DATE: 1998-06-05
PRIOR APPLICATION NUMBER: 60/08023
PRIOR PRICING DATE: 1998-06-05
PRIOR APPLICATION NUMBER: 60/080217
PRIOR APPLICATION NUMBER: 60/080821
PRIOR APPLICATION NUMBER: 60/080821
PRIOR APPLICATION NUMBER: 60/080821
PRIOR PRIOR APPLICATION NUMBER: 60/080821
PRIOR PRIOR APPLICATION NUMBER: 60/080826
PRIOR APPLICATION NUMBER: 60/080821
PRIOR APPLICATION NUMBER: 60/080821
PRIOR APPLICATION NUMBER: 60/080821
PRIOR APPLICATION NUMBER: 60/080821
PRIOR APPLICATION NUMBER:

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RESULT 2
PCT-US91-06532-1/c
; Sequence 1, Application PC/TUS9106532
; GENERAL INFORMATION:
; APPLICANT: Roizman, Bernard
TITLE OF INVENTION: Recombinant Herpes Simplex Viruses
; TITLE OF INVENTION: Vaccines and Methods
; NUMBER OF SEQUENCES: 8
; CORRESPONDENCE ADDRESS:
; CORRESPONDENCE ADDRESS:
; CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                          HILING DALE: 1970.

ATTORNEY/AGENT INFORMATION:
NAME: GTUDEY, LEWIS S.
REGISTRATION NUMBER: 30,060
REGISTRATION NUMBER: 27373
REFERENCE/DOCKET NUMBER: 27373
TELECOMMUNICATION INFORMATION:
TELEFPAN: 312,7946-7740
TELEFPAN: 312,7946-7740
TELEFPAN: 312,7946-7740
TELEFPAN: 312,7946-7740
TELEFYN: 25-3856
INFORMATION FOR SEO ID NO: 1:
SEQUENCE CHARACTERISTICS:
LENGTH: 1335 base pairs
TYPE: NUCLEIC ACID
STRANDEDNESS: Single
TOPOLOGY: Linear
TOPOLOGY: Linear
TOPOLOGY: DNA (genomic)
PCT-US91-06532-1
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PRIOR FILING DATE: 1998-07-07
PRIOR APPLICATION NUMBER: 60/091982
PRIOR FILING DATE: 1998-07-07
PRIOR APPLICATION NUMBER: 60/092182
PRIOR FILING DATE: 1998-07-09
                                                                                                                                                         Query Match 9.0%; Score 49.4; DB 5; Length 1335; Best Local Similarity 48.0%; Pred. No. 0.047; Matches 169; Conservative 0; Mismatches 182; Indels 1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  COUNTRY: USA
ZIP: 60603
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
COMPUTER: IBM PC LOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
SOFTWARE: PatentIn DATA:
CURRENT APPLICATION NUMBER: PCT/US91/06532
ETILING DATE: 19910910
ETILING DATE: 19910910
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ADDRESSEE: Marshall, O'Toole, Gerstein, Murray & ADDRESSEE: Bicknell STREET: Two First National Plaza Suite 2100
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           474 GCGAGGACCGGGTATAAGAAGCCTCGTGGCCTTGCCCGGGCAGGCTGCGAGGTTCCCCGCGC 533
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                                                                                27373/8235
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35	841409	298	238 841349	181 841289	121 841229	61 841169	1 841109	Match Local Similarity es 231; Conser	ER INFO	LENGTH: 44(TYPE: DNA ORGANISM: 1	GE SEE	APPLICANT: TITLE OF IN TITLE OF IN FILE REFERE		24	423 (468 (483	43	349 G	603 C	289 G
8 AGGG								Simila 1; Co	E: INFORMATION: INFORMATION: INFORMATION: 840A-2	4403765 1A 1: Mycobac	PLICATION NUI LING DATE: SEQ ID NOS: PatentIn Ver	: VENTER, INVENTION: INVENTION: RENCE: 243	RMATION: FLEISCHMAN, WHITE, Owe FRASER, Cl	σ.	GITGGGCCGGCCTCTGGCGCCGGCTCGGCGGGGGGGCTGTCCGGCCAGTCG	GGAGGGGCGAGGACCGGGTATAAGAAGCCTCGTGGCCTTGCCCGGGCAGCCG	GTTAGC	CGCAG	GGGCAGGGAAGGGGCTTCCCAGGGCCGCCGCCGCAGCAGGAAGTTGGCCAG 	CGGCGCCCCTCCCCGCCCCGCGCGCGCAGGCGCAGGCGCGCAAGGTGCTCTGCGGTGAC	96000
GGCACO	AGTCGC	ICTCTC	SACCGC	ACCNG CCGGA	ACCAG	AAGGC	GCGGCAC	larity Conservat		acterium	NOS:	IR, John IN: DNA IN: TUB 14366-20	0₽	lication 328	cceec	GAGG	111	CGGAG	GAAGG	CCCTC	
GGGGCACGGGCTTCCCAGGGCCCGCCGGCCGCAGCAGGAAGTTGGCCAGGGC	CGCTAGTCGCAGCGGCGATTCGGCGGGGCAGGCGGAGCCGGCGGCGACGCCGGC	AGAGG	AAAGCC AACGCC	CCCTCACCNGAGGGAAGCTCCCCTCACCCGGCC	GGAGCC GGCGGT	GCCCAC	3666CC	8.9%; 46.7%; ative	CDC 1551 "n" bases represent	um tube	MBER: 1998-0 2 . 2.1	TUBERCULOSIS	3 R		CTCTG	ACCGG	#GCCCGCCCCCGGGCGCGGGCGGTGGGGACCGGGGGGGGGG	CAGGCGGAAGGCGAAGGCGCGACGCGTTTTTTTAGGAGCGGGGC-GAGGCCGGCGCT	GGGCAC	ccccc	- (- (- (- (- (- (- (- (- (- (
CCCAGO	CGGATT	3CCCC#	BAAGGT CGGGAC	AGCTCC	AGGAA	GAGGA	cggga(ggcgg	*; Sc	at a,	perculo)6-24	ENCES LOSIS	. t	US/09103840A	3CGCC6	STATAA	300000	A PLACE	GGGCT	cecec	-
GCCCG	ceece	- GCGCC	GCTCGC	CCTCAC	CTGCGC	CATGCT	TGAGG GGCCTC	Score 4 Pred. N); Mism	variou	osis	/103,0	FOR)A	GCTCG	GAAGC	1 1	C 90000	TCCCAC	GTCGC	- -
cceecc	GGCAG	IGCCAA	CACTG	CCGGC	CGCCCC GGCAG	GTGCC	CACCGA	re 48.8; DB d. No. 0.081; Mismatches	13 00		5	. 4			gecege	TCGTG	GCGGT	4.4.4.C.4.	111	eccc.	=
GCAGC.	GCGGA	GAGGA	TGGGC	CGGGCI	ccecco	CGACGT 	CGTCG	DB 3;)81; ; 253				ANALYS			GGGCT	GCCTT	 GGGA	CAGGA	1 	AGGCGC	=
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CA	ATG	TGCCTCTCTCAGAGGGCCCCAGCGCCTGCCAAGAGGAAGTCCTCGAGGCCCGGGCAGGGA	GTCAGACCGCAAAGCGAAGGTGCGGCCCACGGGGCCTCGCGGAGACAAAGGCCGGCGCGCGGCGGCGGGCG	CCCTCACCNGAGGGAAGGTCCCCTCACCCGGCCCAGCCCTGCAGGGGGGGCCGTGGGGGCCGTGGGGGGGGGCGGGGGGGG	CAGGGACCÁGGGAGCCAGGAACTGCGCCGCCCCCCCCCCC	CGCAGAAAGGCGCCCACGAGGACCCCCAGTGCCCGACGACGTCGGCATCAGAGGCGCGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGG	CGGCCGGGGAGCCGGGAGTGAGGCCTGATCGTCCCTGGCGGCGTCGCGGTGGGGCGG 	Gaps	sequenc			RIUM			8	. 40	ececc 				
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Sequence 16, Application US/09128155

Patent No. 6117654

I Patent No. 6117654

I GENERAL INFORMATION:
APPLICANT: PAN, Yang
ITILE OF INVENTION: NOVEL MOLECULES OF TANGO-77 RELATED PROTEIN FAMILY
FILE REPERENCE: 09404/052001

CURRENT APPLICATION UNMER: US/09/128,155

CURRENT FILING DATE: 1998-08-03

EARLIER APPLICATION UNMER: US 60/091,650

EARLIER APPLICATION UNMER: US 60/054,646

RANLIER APPLICATION UNMER: US 60/054,646

NUMBER OF SEQ ID NOS: 18

SOFTWARE: FASTSEQ for Windows Version 3.0

LENGTH: 152331

TYPE: DNA
ORGANISM: Homo saptens
                                           RESULT 5
US-09-103-840A-1
Sequence 1, Application
Patent No. 6294328
GENERAL INFORMATION:
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NAME/KEY: misc_feature
LOCATION: (1)...(152331)
OTHER INFORMATION: n A
US-09-128-155-16
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US-09-128-155-16/c
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Best Local Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             151;
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                                                                                                                                                                                                                                                                                                                                                            CGGCGCTGGAGGÁGCGAGGACCGGGTATAAGAAGCCTCGTGGCCTTGCCCGGGCAGCCGC 520
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                                                                                                US/09103840A
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Pred. No. 0.079;
0; Mismatches 149; Indels 3;
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RESULT 6
US-08-232-463-14/c
Sequence 14, Application US/08232463
Patent No. 567/367
GEMERAL INFORMATION:
GENERAL INFORMATION:
APPLICANT: SCHELFLINGER, F.
APPLICANT: SCHELFLINGER, F.
APPLICANT: FALKNER, F. G.
INTILE OF INVENTION: RECOMBINANT FOWLPOX VIRUS
CORRESPONDENCE ADDRESS:
CORRESPONDENCE ADDRESS:
ADDRESSEE: FOLEY & Lardner
STREET: 1800 Diagonal Road, Suite 500
CITY: Alexandria
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; ORGANISM: Mycobacterium tuberculosis
; OTHER INFORMATION: H37Rv
US-09-103-840A-1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                APPLICANT: FLEISCHMAN, Robert D.
APPLICANT: WHITE, Owen R.
APPLICANT: WHITE, Owen R.
APPLICANT: VENTER, John C.
TITLE OF INVENTION: DNA SEQUENCES FOR STRAIN ANALYSIS IN MYCOBACTERIUM TITLE OF INVENTION: TUBERCULOSIS
FILE REFERENCE: 24366-20007.00
CURRENT APPLICATION UMBER: US/09/103,840A
CURRENT FILING DATE: 1998-06-24
NUMBER OF SEQ ID NOS: 2
SOCTWARE: Patentin Ver. 2.1
LENGTH: 4411529
TYPET NNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Best Local Similarity Matches 237; Conserv
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        839231 CGCTAGTCGCAGCGGCGGATTCGGCGGGGGCCGGCGGAGCCGGCGACGCGGCATGTT 839290
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                238 GTCAGACCGCAAAGCGAAGGTGCGGGCCGGGGTGGGCCTCGCGGAGACAAAGGCCGGGCC 297
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 61 CGCAGAAGGCGCCCACGAGGACCCCCAGTGCCCGACGTTGCCACGGTCTGGGATCAGAGG 120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       1 CGGCCGGGGAGGCGGGAGTGAGGCCTGATCGTCCCTGGCGCCTCCACCTCCCCAGG 60
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       AGGGGCACGGGCTTCCCAGGGCCCGCCGGCCGCAGCAGGAGGTTGGCCAGGG-CACGGC 416
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       CGCCGGCGGGCCGGGGCCCCCGGGGCTGATCGGCAACGGCGGCAACGGCGGCAACGG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TGCCTCTCAGAGGGCCCCAGCGCCTGCCAAGAGGAAGTCCTCGAGGCCCGGGCAGGGA 357
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              GGCCGGCGAACGCCGGGACACTCGCCACTGGTGATGGCGGGGCCGGGGGACCGGCGG 839230
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       CAGGGACCAGGAGCTGCGCCCCCCCCCCCCCCCCTGCCCTTGCCCTTGCGCGAGGGAAGCT 180
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Pred. No. 0.097;
0; Mismatches 247; Indels 11;
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237 839170

838990

839410

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; CLONE: pTZgpt-F1s
US-08-232-463-14
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PRIOR APPLICATION DAMBER: US/07/935,313
APPLICATION NUMBER: EP 91 114 300.6
APPLICATION NUMBER: EP 91 114 300.6
APPLICATION NUMBER: EP 91 114 300.6
FILING DATE: 26-AUG-1991
ATTORNEY/AGENT INFORMATION:
NAME: BENT, Stephen A.
REGISTRATION UNMBER: 30472/114 IMPREFERENCE/DOCKET NUMBER: 30472/114 IMPREFERENCE/TOOKET NUMBER: 30472/114 IMPREDIANT ON FOR SEQ ID NO: 14:
TELEPAN: (703)836-9300
TELEPAN: (703)836-9300
TELEPAN: (703)683-4109
TELEY (703)836-9300
TELEPAN: 10368-4109
TYPE: DATA CONTRELISTICS:
LENGTH: 71218 Dase pairs
TYPE: DATA CONTRELISTICS:
LENGTH: 71218 Dase pairs
TYPE: DATA CONTRELISTICS:
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                                                                                                                                                                                               RESULT 7
US-08-458-912-1/c
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Best Local S
Matches 13
                                                                                                              Sequence 1, Application US/08458912
Patent No. 5650310
GENERAL INFORMATION:
APPLICANT: Broer, Inge
APPLICANT: Hillemann, Doris
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version
CURRENT APPLICATION DATA:
                                                                              APPLICANT:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             STATE: VA
COUNTRY: USA
ZIP: 22313-0299
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              APPLICATION NUMBER: FILING DATE:
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                                                     APPLICANT:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Watch 8.6%; Score 47.2; DB 1;
Local Similarity 4.4%; Pred. No. 0.14;
hes 13; Conservative 171; Mismatches 114;
                                                                                                                                                                                                                                                                                                                             1159
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                                                                                                                                                                                                                                                                                                                                                                                                                       283 GACAAAGGCCGGGCCTGCCTCTCTCAGAGGGCCCCAGCGCCTGCCAAGAGGAAGTCCTCG 342
                                                                                                                                                                                                                                                                                             463
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USA
ANT: Mullner, Hubert
ANT: Bartsch, Klaus
Trivention: DF?
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                                                                                                                                                                                                                                                              GCGCTGGAGGGCGAGGACCGGGTATAAGAAGCCTCGTGGCCTTGCCCGGGCAGCCGC 520
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                        Klaus
DEACETYLASE GENES FOR THE PRODUCTION
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TOPOLOGY:
US-08-458-912-1
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TELECOMMUNICATION INFORMATION:
TELEPHONE: (212) 840-0712
INFORMATION FOR SEQ ID NO: 1:
SEQUIENCE CHARACTERISTICS:
LENGTH: 932 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
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RESULT 8
US-08-461-179-1/c
US-08-461-179-1/c
; Sequence 1, Application US/08461179
; Patent No. 5668297
; GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ZIP: 1036

COMPUTER READABLE FORM:

COMPUTER READABLE FLOPPY disk

MEDIUM TYPE: Floppy disk

COMPUTER: IBM PC COMPATIBLE

COMPUTER: IBM PC COMPATIBLE

COPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: PATENTIN Release #1.0, Version #1

CURRENT APPLICATION DATA:

APPLICATION UNUMBER: US/08/458,912

FILING DATE: 02-JUN-195

CLASSIFICATION: 435

CLASSIFICATION: 435

PRIOR APPLICATION UNMBER: US 07/926,498

APPLICATION NUMBER: US 07/926,498

ETLING DATE: 07-AUG-1992

ATTORNEY/AGENT INFORMATION:

NAME: LOWERICE, WILLIAM F.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Query Match
Best Local
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Matches
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TITLE OF INVENTION: PHO
TITLE OF INVENTION: PRO
TITLE OF SEQUENCES: 1
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ADDRESSEE: Curtis, Morris & Safford ADDRESSEE: c/o William F. Lawrence STREET: 530 Fifth Avenue CITY: New York STATE: New York COUNTY: United States of America COUNTY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     184 TCACCNGAGGGAAGCTCCCCTCACCCGGCCCAGCCCTGCAGGGGGGGCGCGCTGGGGTCAGA 243
                                                                                                                                                                                                                                                                                                                                                                                             744 TOGTCGTACAGGACTTCCTCGGAACCGACCTGGATGAGCAGGGGGGGCAGACCGGTCAGA 685
                                                                                                                                                                                                                                                                                                                              624
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                h 8.5%;
Similarity 48.5%;
64; Conservative (
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                                                                                                                                                                                                                                                           TCACCGGCGAAGGTGATCCGCCCCGGCGGCAGGCCCCG
                                                                                                                                                     CGAGGACCGGGTATAAGAAGCCTCGTGGCCTTGCCCGG 512
                                                                                                                                                                                                                          GGAG-------CGGGCAGGGCTTTCTCAGGAGCGCGGGCGAGGCCGGCGCTGGAGGGG 474
                                                                                                                                                                                     PHOSPHINOTHRICIN OR PHOSPHINOTHRICYL-ALANYL-ALANINE, PHOSPHINOTHRICYL-ALANYL-ALANINE, PROCESSES FOR THEIR ISOLATION, AND THEIR USE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          0;
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Pred. No. 0.17;
0; Mismatches 165;
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APPLICANT:

Doris

STREET: 530 STREET: New York
STATE: New York
Traited S

COUNTRY: U

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APPLICATION NUMBER: US/08/461,179
CLASSIFICATION 435
PRIOR APPLICATION DATA.
APPLICATION DATA.
APPLICATION NUMBER: US 07/926,498
FILING DATE: 07-AUG-1992
ATTORNEY/AGENT INFORMATION:
NAME: LAWTENCE 28,029
REFERENCE/DOCKET NUMBER: 514410-2887
REGISTRATION INFORMATION:
TELEPHONE: (212) 840-3333
TELEFAX: (212) 840-0712
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERIFICS: 1
SEQUENCE CHARACTERIFICS: 1
SEQUENCE CHARACTERIFICS: 517PE: NUCLEAC acid
STRANDEDNESS: $1101e
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MEDIUM TYPE: Floppy disk
COMPUTER: IBM PER POLYMONIC POLYMONIC
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APPLICANT: Mullnet, Hubert
APPLICANT: Bartsch, Klaus
TITLE OF INVENTION: DEACETYLASE GENES FOR THE PRODUCTION OF
TITLE OF INVENTION: PHOSPHINOTHRICIN OR
TITLE OF INVENTION: PHOSPHINOTHRICYL-ALANYL-ALANINE,
TITLE OF INVENTION: PROCESSES FOR THEIR ISOLATION, AND THEIR USE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ADDRESSEE: Curtis, Morris & Safford ADDRESSEE: C/O William F. Lawrence STREET: 530 Fifth Avenue
                                         475 CGAGGACCGGGTATAAGAAGCCTCGTGGCCTTGCCCGG 512
                                                                                                                                                                                                                                                                                                                                                                                                                                                                         GAGGCGCCCTCGCAGGCCAGGTCGGCCCAGGGCGAGATGCACACCGCGGCGGCGGCAGC
                                                                                                                                                                                                                                                                       TCTCAGAGGGCCCCAGCCCAGCCAAGAGGGAAGTCCTCGAGGCCCGGGCAGGGAAGGGGG
                                                                                                                                                                                                                                                                                                                                   GCCATGCGGAGCAGGTCCTCGGTGTCCAGGAGGATCTCGCGCCTCCTTGCGGGTGACGTGC
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ilarity 48.5%;
Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Score 46.6; DB 1; Length 932; 
Pred. No. 0.17;
0; Mismatches 165; Indels 9;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 514410-2882
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MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-POS
SOFTWARE: PATENTH Release #1.0, Vers
APPLICATION DATA:
APPLICATION NUMBER: US/08/459,254
FILING DATE: 02-JUN-1995
PRIOR APPLICATION UNDER: US 07/926,498
FILING DATE: 07-AUG-1992
PRIOR APPLICATION NUMBER: US 07/926,498
APPLICATION NUMBER: US 07/926,498
APPLICATION NUMBER: 28,029
ATTORNEY/AGENT INFORMATION:
NAME: Lawrence, William F.
REGISTRATION NUMBER: 514410-288;
PRICOMMUNICATION INFORMATION:
TELEPHONE: (212) 840-333
INFORMATION FOR SEO ID NO: 1:
SEQUENCE CHARACTERISTICS:
LENGTH: 932 base pairs
TYPE: nucleic acid
CTTANNIPLESS: Single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        US-08-459-254-1
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Best Local Similarity 48.5

Matches 164; Conservative
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US-08-459-254-1/c
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APPLICANT: BARTSCH, KLAUS
TITLE OF INVENTION: DEACETYLASE GENES FOR THE PRODUCTION OF
TITLE OF INVENTION: PHOSPHINOTHRICIN OR
TITLE OF INVENTION: PHOSPHINOTHRICYL-ALANYL-ALANYNE,
TITLE OF INVENTION: PHOSPHINOTHRICYL-ALANYL-ALANYNE,
TITLE OF INVENTION: PROCESSES FOR THEIR ISOLATION, AND THEIR
UNMBER OF SEQUENCES: 1
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   COUNTRY: U
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CITY: New York
STATE: New York
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ADDRESSEE: Curtis, Morris & Safford ADDRESSEE: C/O William F. Lawrence STREET: 530 Fifth Avenue
364 CACGGGCTTCCCAGGGCCCGCCGGCCGCAGGAGGAGGTTGGCCAGGGCACGCCGTTGAGC
                                                                                                                                                                                    624 GCCATGCGGAGCAGGTCCTCGGTGTCCAGGAGGATCTCGCGCTCCTTGCGGGTGACGTGC
                                                                                                                                                                                                                                                                                                                             304
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                                                                                                                              TCTCAGAGGGCCCCAGCGCCTGCCAAGAGGAAGTCCTCGAGGCCCGGGCAGGGAAGGGGG
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ANT: Broer, Inge
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 l, Application US/08459254
o. 5767370
                                                                                                                                                                                                                                                                                       New York
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Wohlleben, Wolfgang
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                                                                                                                                                                                                                                                                                                                                                                                                            8.5%; Score 46.6; DB 1;
48.5%; Pred. No. 0.17;
ative 0; Mismatches 165;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Gunter
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US-08-461-179-1

STRANDEDNESS:

linear

Query Match Best Local Similarity Matches 164; Conserv

Qy Дb Qy Дb δõ DЬ Q В δÃ

us-10-081-817a-19.rni

INFORMATION FOR SED ID NO: 1: SEQUENCE CHARGTERISTICS: LENGTH: 932 base pairs TYPE: nucleic acid STRANDEDNESS: single TOPOLOGY: linear US-08-459-255-1 B.5%; Score 46.6; DB 1; Length 932; Query Match Best Local Similarity 48.5%; Pred. No. 0.17; Best Local Similarity 48.5%; O; MCIGGCCCAGCCTGCAGGGGGGGGGGTCAGA 243 Matches 164; Conservative 0; MCIGGCCCAGCCTGCAGGGGGGGGGGGTCAGA 243 MAtches 164; Conservative 1 1 1 1 1 1 1 1 1 1	HELET GALLON TOLL	1 1 SS: SS: Norris & Safford Iliam F. Lawrence 1 Avenue 1 Avenue 1 States of America STATE OF AMERICA	PATENT NO. 37077101: GENERAL INFORMATION: GENERAL INFORMATION: APPLICANT: Hillemann, Doris APPLICANT: Hollemann, Doris APPLICANT: Publier, Alfred APPLICANT: Donn, Gunter APPLICANT: Donn, Gunter APPLICANT: Mullner, Hubert APPLICANT: Mulln	444 444 425 3-255	Mon Sep 22 15:31:38 2003 Mon Sep 22 15:31:38 2003 b 564 GAGGCGCCTCGCAGGCCAAGGCCAAGGCGAAGACCGCGGCGGCGAGGC 505 Db 424 GGAGCGGGCAAGGCTTTCTCAGGAGCGCGAAGGCCGGCGCGCGC
; MOLECULE TYPE: CDNA US-08-586-165-8 Query Match Best Local Similarity 48.1%; Pred: No. 0.22; Indels 2; Gaps 1, Best Loca	APPLICATION NUMBER: 05/07/07/07/07/07/07/07/07/07/07/07/07/07/	Brook, Smith & Reynolds, F. Drive prive s disk mpatible mpatible mc-DOS/MS-DOS Release #1.0, Version #1.30 Release #1.0, Version #1.30 VIA: WO 156 155	SULT 11 108-586-165 Sequence 8, Patent No. GENERAL IN APPLICAN APPLICAN APPLICAN APPLICAN APPLICAN APPLICAN APPLICAN	424 GGAGCGGGCAGGGCTTTCTCAGGAGGCCGGGCGAGGCCGGCGAAGGCTATACAAGAAGCCTCGGCCGGC	Db 684 TCGCCGTGGGCGAGGCCAGGGGGTTCCTGGGATCGGTGCCGGCAGGTAGCGCCCC 625 Db 304 TCTCAGAGGGCCCAGCGCCTGCCAAGAGGAAGTCCTCGAGGCCAGGGAAGGGGG 363 Qy 1

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COMPUTER READABLE FORM:

MEDIUM TYPE: Flòppy disk
COMPUTER: IBM PC COMPATIBLE
COMPUTER: IBM PC COMPATIBLE
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/814.095
FILING DATE:
CLASSIFICATION: |800
ATTORNEY/AGENT INFORMATION:
NAME: MONTGOMERY, ILENE 38,972
REFERENCE/DOCKET NUMBER: 2391.00066
TELECOMMUNICATION INFORMATION:
TELEPHONE: (248) 539-5055
INFORMATION FOR SEQ ID NO: 7:
SEQUENCE CHARACTERISTICS:
LENGTH: 35060 base pairs
TYPE: nucleic acid
STRANDEDNESS: double
TOPOLOGY: linear |
MOLECULE TYPE: other nucleic acid
DESCRIPTION: /desc = "Cosmid including ACHE
DESCRIPTION: promotor, ACHE gene and ARS gene"
HYPOTHETICAL: NO
ORIGINAL SOURCE:
OPERATION SOURCE: Nome and line
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    B
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US-08-814-095-7
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              В
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Sequence 7, Application US/08814095
Patent No. 6025183
GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       APPLICANT: Zakut, Haim
APPLICANT: Shani, Mosima
TITLE OF INVENTION: TRANSGENIC ANIMAL ASSAY SYSTEM FOR
TITLE OF INVENTION: ANTI-CHOLINESTERASE SUBSTNACES
NUMBER OF SEQUENCES: 7
                                                                                                                                                                                                                   ORGANISM: Homo sapiens POSITION IN GENOME:
                                                                                                                                                                 CHROMOSOME/SEGMENT:
FEATURE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           CORRESPONDENCE ADDRESS:
                                                    NAME/KEY: promoter LOCATION: 4089..22464
OTHER INFORMATION: /function= "ACHE promotor"
OTHER INFORMATION: //standard_name= "ACHE Promotor"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ADDRESSEE: KOHN & ASSOCIATES
STREET: 30500 No. 6025183thwestern Highway, Suite
CITY: Farmington Hills
STATE: Michigan
           NAME/KEY: exon
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          COUNTRY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   155
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              CTGCGCGGCCAGCCTCATGGCCCCCGGGAGCCCCGCG 119
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TTGCCCGGGCAGCCGCAGGTTCCCCGCGCGCCCCCGAG 541
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      GGAGCGCGGGCGAGGCCCTGGAGGGCCGAGGACCGGGTATAAGAAGCCTCGTGGCC 504
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TGTCCCCGGGGCGAGCAGCAGCAGGAGAACGGCGGCGGCGGTGACGGACAGCAGGAAGCA 216
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       7q22
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                                                                                                                                                                               FEATURE:

NAME/KEY: complement (34528..34895)
LOCATION: complement (34528..34895)
OTHER INFORMATION: /function= "arsenit
OTHER INFORMATION: gene"
OTHER INFORMATION: /gene= "AR"
OTHER INFORMATION: /number= 1
FEATURE:
NAME/KEY: exon
LOCATION: complement (34092..34358)
OTHER INFORMATION: /gene= "AR"
OTHER INFORMATION: /number= 2
FEATURE:
NAME/KEY: exon
LOCATION: complement (33779..33963)
OTHER INFORMATION: /gene= "AR"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         NAME/KEY: exon
LOCATION: 28008..28129
LIDENTIFICATION METHOD: experimental
LOTHER INFORMATION: /evidence= EXPERIMENTAL
OTHER INFORMATION: /gene= "ACHE"
OTHER INFORMATION: /number= 6
FEATURE:
NAME/KEY: terminator
LOCATION: 28129..28131
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  IDENTIFICATION METHOD:
OTHER INFORMATION: /evi
OTHER INFORMATION: /ger
OTHER INFORMATION: /nun
FEATURE:
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LOCATION: 27255..28007
LDENTIFICATION EXTHUD: experimental
DOTHER INFORMATION: /evidence- EXPERIMENTAL
OTHER INFORMATION: /gene- "ACHE"
OTHER INFORMATION: /number= 5
FEATURE: terminator
NAME/KEY: terminator
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NAME/KEY: exon
LOCATION: 25524..26009
LDENTIFICATION METHOD: experimental
OTHER INFORMATION: /evidence= EXPERIMENTAL
OTHER INFORMATION: /gene= "ACHE"
OTHER INFORMATION: /number= 3
FEATURE:
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NAME/KEY: eXON
LOCATION: 24090..25177
LOCATION: 24090..25177
LOCATION: 24090...
OTHER INFORMATION: /function= "(translation start:
OTHER INFORMATION: 24110)"
OTHER INFORMATION: /evidence= EXPERIMENTAL
OTHER INFORMATION: /function= "ACHE"
OTHER INFORMATION: /function= "ACHE"
OTHER INFORMATION: /fundber= 2
                                                                                  LOCATION: complement (33493..33591)
OTHER INFORMATION: /gene= "AR"
OTHER INFORMATION: /number= 4
FEATURE:
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OTHER INFORMATION: /function= "non-translated"
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NAME/KEY: exon
LOCATION: complement (33297..33408)
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LOCATION: 27005..27274
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       IOD: experimental
  /evidence= EXPERIMENTAL
  /gene= "ACHE"
  /number= 4
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        /function= "arsenite resistance
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/number=

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NAME/KEY: exon
LOCATION: complement (29664..29856)
OTHER INFORMATION: /gene= "ARS"
OTHER INFORMATION: /number= 16
US-08-814-095-7
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                                                                                                                                                                             QΥ
                          δ
                                                                 Вþ
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Best Local Similarity 46.8%;
Matches 176; Conservative
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LOCATION: complement (30816..31011)
OTHER INFORMATION: /gene= "AR"
OTHER INFORMATION: /number= 12
FEATURE:
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EATURE:
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OTHER INFORMATION: /gene= "AR"
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OTHER INFORMATION: /gene= "AR"
OTHER INFORMATION: /number= 8
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LOCATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     EATURE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     NAME/KEY: exon
LOCATION: complement (31894...32080)
OTHER INFORMATION: /gene= "AR"
OTHER INFORMATION: /number= 9
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LOCATION: complement (31363..31534)
OTHER INFORMATION: /gene= "AR"
OTHER INFORMATION: /number= 10
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LOCATION: complement (30470...30626)
OTHER INFORMATION: /gene= "AR"
OTHER INFORMATION: /number= 13
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LOCATION: complement (31131..31284)
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OTHER INFORMATION: /number= 11
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  NAME/KEY: exon
LOCATION: complement (30187..30274)
OTHER INFORMATION: /gene= "AR"
OTHER INFORMATION: /number= 14
                                                                                                                                                                                                                                                                                                                                                                                                        LOCATION: complement (29945..30073)
OTHER INFORMATION: /gene= "AR"
OTHER INFORMATION: /number= 15
                                                                                                                                                                                                                                                                                                                                                                                                                                                                   NAME/KEY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  CATION: complement (32569..32628)
HER INFORMATION: /gene= "AR"
HER INFORMATION: /number= 7
                                                                                                                                            28385 CAGAACGCCGGAATCACGGGGGGCCGAGTCTATGCAGGAGCGGGGCTGGAGGGCAAGAAAC 28444
                                   271 GGGCCTCGCGGGGAGACAAAGGCCGGGCCTGCCTCTCTCAGAGGGGCCCCAGCGCCTGCCAAG 330
                                                                        GCTGCCAATAAACTGTTACAGCCACGGGAGTGTGCGCGACTAGGGACCCAGGGGTAGAGG
                                                                                                GCCCAGCCCTGCAGGGGGGGCGCGTGGGGTCAGACCGCAAAGCCGAAAGGTGCGGGCCCGGGGT 270
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                                                                                                                                                                                                                           Score 45.8; DB 3;
Pred. No. 0.28;
0; Mismatches 198;
                                                                                                                                                                                                                                 198;
                                                                                                                                                                                                                                                                    Length 35060;
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210

28324

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                                                                                                         STRANDEDNESS:
TOPOLOGY: line
MOLECULE TYPE: 1
US-08-483-533-4
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US-08-483-533-4
                                                                                                                                              TELLER: 314,
TELLER: 25-3856
TELER: 25-3856
TELER: 25-3856
INFORMATION FOR SEQ ID NO: 4:
SEQUENCE CHARACTERISTICS:
SEQUENCE CHARACTERISTICS:
LENGTH: 595 base pairs
TYPE: nucleic acid
TYPE: nucleic acid
               δõ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Patent No.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Sequence 4,
                                                Query Match
Best Local S
Matches 183
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ZIF: 60000 717-
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      APPLICANT: Chou, Joany
APPLICANT: Chou, Joany
TITLE OF INVENTION: Method for Treating Tumorigenic
TITLE OF INVENTION: Diseases
NUMBER OF SEQUENCES: 43
CORRESSPONDENCE ADDRESS:
ADDRESSE: Marshall, O'Toole, Gerstein, Murray &
STREET: 6300 Sears Tower, 233 South Wacker Drive
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SOFTWARE: Patentin Rel CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                             PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/419,853
FILING DATE: 11-APR-95
PRIOR APPLICATION DATA:
PAPPLICATION NUMBER: 07/861,233
FILING DATE: 31-MAR-92
                                                                                                                                                                                                                                                              NAME: Zeller, James P.
REGISTRATION NUMBER: 28.491
REFERENCE/DOCKET NUMBER: 28
REFERENCE/TOOKET NUMBER: 28
TELECOMMUNICATION INFORMATION:
TELECHMONE: 312/474-6300
TELEFAX: 312/474-0448
                                                                                                                                                                                                                                                                                                                                             FILING DATE: 31-MAR-92
ATTORNEY/AGENT INFORMATION:
NAME: Zeller, James P.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                        APPLICATION NUMBER: US. FILING DATE: 07-MAR-95 CLASSIFICATION: 514
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         STREET: 6300 :
CITY: Chicago
STATE: Illino
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 28445 AGGCGAGCTCCGAGGCGGGCGCAAGGCAAAGGCCAACCCCTAGCCCTGCCCTGCCGGGCG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      COUNTRY: United States of America ZIP: 60606-6402
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    28565
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  28505 GAGCTCGCGCCTGCGTAATGAGGCCCGCAGGCAGGCTAGCTGGCACGCGGAGGGGAGGA 28564
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    28625 CTCGGTCGGTGCCGGT 28640
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              449
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     509
                                              tch 8.2%; al Similarity 46.2%; 183; Conservative
23 TGAGGCCTGATCCTGGCGGCCTCCACCTCCCCAGGCGCAGAAAGGCGCCCCACGAGAC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  CGCGGGCGAGGCCGCGCGTGGAGGGGCGAGGACCGGGTATAAGAAGCCTCGTGGCCTTGC 508
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       CCGGGCAGCCGCAGGT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Roizman, Bernard
                                                                                                                             linear
E: DNA (genomic)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              US/08/483,533
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                                                                                                                                                                                                                                     4:
                                                   Score 45:4; DB 3;
Pred. No. 0.3;
0; Mismatches 212;
                                                                                                                                                                                                                                                                                                                  28097/32742
                                                                                        Length 595;
                                                           Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Borun
                                                             1;
                                                             Gaps
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                                82
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COMPUTER READABLE FORM:

MEDIUM TYRE: Plopby disk
COMPUTER: IBM PC COMPUTER: IBM PC COMPUTER: OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
APPLICATION NUMBER: US/09/283,471A
FILING DATE: 04-APR-1999
CLASSIFICATION DATA:
APPLICATION NUMBER: 10/861,233
FILING DATE: 31-MAR-1992
PRIOR APPLICATION NUMBER: 08/419,853
FILING DATE: 11-APR-1995
PRIOR APPLICATION NUMBER: 08/419,853
FILING DATE: 07-JUN-1995
APPLICATION NUMBER: 08/483,533
APPLICATION NUMBER: 28/491
REFERENCE/DOCKET NUMBER: 28/491
REFERENCE/DOCKET NUMBER: 27/373/32742A
TELLEFAX: 31/474-0448
TELLEFAX: 31/474-0448
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            RESULT 14
US-09-283-471A-4
                                                        TELEX: 25-3856
INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Sequence 4, Application US/09283471A Patent No. 6340673
GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    APPLICANT: Roizman, Bernard
APPLICANT: Chou, Joany
TITLE OF INVENTION: Method For Treating Tumorigenic Diseases
NUMBER OF SEQUENCES: 43
CORRESPONDENCE ADDRESS:
ADDRESSE: Marshall, O'Toole, Gerstein, Murray & Borun
STREET: 6300 Sears Tower, 233 South Wacker Drive
CITY: Chicago |
CITY: Chicago |
STATE: Illinois |
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              COUNTRY: United States of America
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           410 Teccresecces AGECCCGTGCCCGGCCCTGGCC 445
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             350 CGGGCCGACCGGGCTCGGTTCCGGCGGCGCGGGTGGCGGAGGCCGAGGCGGTCATCGGGCCG 409
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       290 CACCTGGTGGTCTGGGCCTCGGCCGCCCTGGCGCGCGCGGCTCGTGGGCCCGCGAG
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US-08-483-533-36
        COUNTRY: United States of America
ZIP: 60606-6402
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC COMPATIBLE
COMPUTER: IBM PC COMPATIBLE
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PATENTICATION DATA:
APPLICATION NUMBER: US/08/483,533
FILING DATE: 07-MAR-95
CLASSIFICATION NUMBER: 08/419,853
FILING DATE: 11-APR-95
PRIOR APPLICATION NUMBER: 08/419,853
FILING DATE: 11-APR-95
PRIOR APPLICATION NUMBER: 07/861,233
FILING DATE: 11-APR-95
PRIOR APPLICATION NUMBER: 07/861,233
FILING DATE: 11-ARR-92
ATTORNEY/AGENT INFORMATION:
NAME: Zeller, James P.
DECTTORNETY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Дb
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; TOPOLOGY: linear
; MOLECULE TYPE: DNA (genomic)
US-09-283-471A-4
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Sequence 36, Applicat Patent No. 6172047 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                        STREET: BougesTREET: BougesTRE: Chicago
STATE: Illinois
COUNTRY: United States of America
ZIP: 60606-6402
ZIP: 60606-6402
CORADABLE FORM:
                                                                                                                                                                                                                                                                                                                                                                                                                                        APPLICANT: ROizman, B
APPLICANT: Chou, Joan
TITLE OF INVENTION: M
TITLE OF INVENTION: D
INUMBER OF SEQUENCES:
CORRESPONDENCE ADDRESS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Matches
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Best Local S
NAME: Zeller, James REGISTRATION NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                     DRRESPONDENCE ADDRESS:
ADDRESSEE: Marshall, O'Toole,
STREET: 6300 Sears Tower, 233
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   350
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183; Conservative
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6172047
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Joany
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Method for Treating Tumorigenic
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Pred. No. 0.3;
0; Mismatches 212;
                                                                                                                                                                                                                                                                                                                                                                                                   Gerstein, Murray &
South Wacker Drive
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Length 595;
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229 202 169 109 82

349 321 289 Qy Qy Qy

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REFERENCE/DOCKET NUMBER: 28097/32742

TELECOMMUNICATION INFORMATION:
TELEPHONE: 312/474-6300
TELEFAX: 312/474-648
TELEX: 25-3856
INFORMATION FOR SEQ ID NO: 36:
SEQUENCE CHARACTERISTICS:
LENGTH: 1327 base pairs
TYPE: nucleic acid
TYPE: nucleic acid
STRANDENNESS: single
TOPOLOGY: linear
MOLECULE TYPE: DNA (genomic)
US-08-483-533-36
                                                                                                                                                                                                                                                               QY
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Search completed: September 20, 2003, 01:41:14 Job time: 89.9316 secs
                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Query Match 8.2%; Score 45.4; DB 3; Length 1327; Best Local Similarity 46.2%; Pred. No. 0.31; Matches 183; Conservative 0; Mismatches 212; Indels 1;
                                                                                                                                                                                                                                                                                                                                                                                                                   203 CTCACCCGGCCCAGCCCTGCAGGGGGGGGGGGGGTCAGACCGCAAAGCGAAAGCGAAGGTGCGG 262
671 ACCCCCGCGAACCCCCGCGACCCCCGCGCGGGGGGGGGTGCGCTTCTCGCCCCACGTCCGGGTGCGC 730
                                                                                                                                                                                                                                                                                               791
                                                                                                                                                                             TGCCTGGGGCCCGAGGCCCGTGCCCGGGCCCTGGCC 886
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                                                                                                                                      CCTGCCAAGAGGAAGTCCTCGAGGCCCGGGCAGGGAAGGGGGCACGGGCTTCCCAGGGCC 381
                                                                                       CGCCGGCCGCAGCAGGAAGTTGGCCAGGGCACGGCC 417
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Title: Perfect score: Sequence:

US-10-081-817A-19 551 1 cggccggggaggcgg

cggccggggaggcggccggg.....gcgccccgagccccgcgcc 551

Scoring table:

IDENTITY_NUC Gapop 10.0 ,

Gapext 1.0

Minimum DB seq length: 0 Maximum DB seq length: 2000000000

of

hits satisfying chosen parameters:

2552756 seqs, 1349719017 residues

Post-processing: Minimum Match
Maximum Match

Listing first 45 summaries

100%

Database

Result Ö

Score

Query Match

Length

DB

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Description

pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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1794 562 190 543 543 519 569 570

ABT06542 AAV54620 AAV54616 AAZ98173 AAZ29723 AAZ29723 AAV54621 ABK40267 AAZ65103

Membrane-bound pro

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nucleic search, using sw

Copyright

GenCore version 5.1.6 (c) 1993 - 2003 Compugen Ltd

September 19,

2003,

23:14:28; model

28; Search time 259.219 Seconds (without alignments) 5737.968 Million cell updates/sec

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Human HIN-1 coding LU105 specific con LU105 specific pol Human signal pepti Human lung specific LU105 polypeptide cDNA encoding human
RESULT 1
ARTO6542
ID ABF0
XX
XX
ARTO6542
AC ABF0
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                                                                                                                                                                                                                                                                                                                                                  Human; methylated gene; methylation; breast cancer; marker; WT-1; cell proliferative disorder; TWIST; HOXA5, NES-1; RABbeta; cyclin D2; retinoic acid receptor beta; cestrogen receptor; Wilms' tumour; 14.3.3 signa; HIN-1; RASSFIA; tumour suppressor gene; hypermethylation; gene; promoter; ds.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Human HIN-1 coding sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      07-NOV-2002
                                                                                                                                                                                                                        01-AUG-2002.
                                                                                                                                                                                                                                                                    WO200259347-A2.
                                                                                                                                                                                                                                                                                                                   Homo sapiens.
                                                                                      (UYJO ) UNIV JOHNS HOPKINS SCHOOL MEDICINE.
                                                                                                                               26-JAN-2001; 2001US-0771357
                                                                                                                                                                              28-JAN-2002; 2002WO-US02455
  WPI; 2002-599803/64.
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11.6 43058
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10.5 114955
10.1 629
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10.2 3743
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ABX77974

ABX79570

ABX64209

ABX17173

ABX164209

ABX17173

ABY54617

ABF10080

AAX53491

ABH64982

ABH64982

ABH64945

ABH643491

ABW621491

ABW621491

ABW621404

AAW621404

AAW6217404

AAW623295
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ABX80386
ABX80890
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                                                      Sacchi N,
                                                         Davidson
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Lullo5 specific pol
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Gene #3953 used to
Lung cancer relate
Human adenosine Al
Oligonucleotide fo
Oligonucleotide fo
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HSV-2 strain SB5 C
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HSV-1 (F) ICP34.5
HUMAN SECRETION TOWN
MYCODACTETION TUDE
HSV-1 IN-178 BAC C
MYCODACTETION TUDE
HSV-1 IN-178 BAC C
MYCODACTETION TUDE
HSV-1 (MGH-10) ICP
Human herpesvirus
HSV-1 (MGH-10) ICP
Human protein Kina
Human low density
Human suff? genomi
Human suff? genomi
Human suff? genomi
Human scolon cancer
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RESULT 2
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    The present invention relates to a method of diagnosing a cellular CC proliferative disorder of breast tissue, which involves determining the CC state of methylation of one or more nucleic acids isolated from the CC subject, where the state of methylation of the nucleic acids as compared CC with a state of methylation from a subject not having the cellular CC proliferative disorder of breast tissue is indicative of a cellular CC proliferative disorder of breast tissue in the subject. The nucleic acids constructed by the cellular CC constructed by the cellular CC constructed by the cellular cCC constructed by the cellular cCC constructed by the cellular cCC constructed by the cellular proliferative disorder including cuctal carcinoma in situ, lobular carcinoma, tubular carcinoma, medullary carcinoma, metaplastic colloid carcinoma, tubular carcinoma in situ, lobular carcinoma in situ and cCC colloid carcinoma, tipular carcinoma in situ, lobular carcinoma in situ and cCC colloid carcinoma, tipular carcinoma in situ, lobular carcinoma in situ and cCC colloid carcinoma in situ. The present sequence is a gene fragment used cCC in the exemplification of the invention.
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Best Local :
Key
                                                                                                                 LU105; lung disease marker; blood; plasma; serum; ss.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Diagnosing and/or determining a predisposition to a cellular proliferative disorder of breast tissue, in particular breast cancer, by determining the state of methylation of one or more nucleic acids isolated from the subject
                                                           Homo sapiens.
                                                                                                                                                                                                    LU105 specific consensus polynucleotide sequence
                                                                                                                                                                                                                                                                25-MAR-2003
30-OCT-1998
                                                                                                                                                                                                                                                                                                                                                                                                                  AAV54620 standard;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Sequence 1794 BP; 240 A; 646 C; 522 G; 318 T; 68 other;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   CTGGAGGGGCGAGGACCGGGTATAAGAAGCCTCGTGGCCTTGCCCGGGCAGCCGCAGGTT 525
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(first entry)
   Location/Qualifiers
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                                                                                                                                                                                                                                                                                                                                                                                                                  562
                                                                                                                                                  immunoassay;
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                                                                                                                                               lung disease; cancer;
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RESULT 3
AAV54616
ID AAV5
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AC AAV5

AAV54616 standard; cDNA; 190

AAV54616;

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                                                                                                                                                Sequences shown in AAV54616 to AAV54621 represent LU105 specific
CC polynucleotide sequences. These are used in the method of the invention
CC for detecting target LU105 nucleic acid. The method comprises treating a
CC sample with at least one LU105 specific nucleic acid, or its complement
CC which is at least 50 percent identical with the LU105 specific nucleic
CC acid sequences (AAV54616 to AAV54621). LU105 is a lung disease marker.
CC cells transformed with a recombinant expression system that contains
CC LU105 specific nucleic acid fragments, are used to express recombinant
CC LU105 specific nucleic acid fragments, are used to express recombinant
CC used to detect the LU105 antigen, and correspondingly this antigen is
CC used to detect specific antibodies, in usual immunoassays. The LU105
CC used to detect specific antibodies, in usual immunoassays staging,
CC monitoring, prognosis, prevention, treatment and determination of
CC susceptibility to, lung disease, specifically cancer. The LU105
CC concentration, in altered form or in an unusual body compartment). LU105
CC can be detected in blood, plasma or serum in an inexpensive, non-invasive
                                                                         Query Match
Best Local S
Matches 120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 New nucleic acid for the lung disease marker LU105 - polypeptides, antibodies and genes, used for diagnosis, prevention, treatment of lung disease, specifically cancer
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P-PSDB; AAW75868.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Billing-medel PA, Cohen Granados EN, Hodges SC, Russell JC, Stroupe SD;
                                                                                                                                                Sequence 562 BP; 82 A; 200 C; 192 G; 86 T; 2 other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Claim 11;
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                                                                                                                                                                            (Updated on 25-MAR-2003 to correct PI field.)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      (ABBO)
120;
                                                                       21.8%; Score 120; DH 19; Length 562; Similarity 99.2%; Pred. No. 1.1e-14; 20; Conservative 0; Mismatches 1; Indels
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/*tag= a

/transl_except= (pos:176..178, aa:Val)

/product= "LU105 polypeptide"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    M, Colpitts TL, Friedman PN, Gordon J; Klass MR, Kratochvil JD, Robertsrapp L;
                                                                         0;
                                                                         Gaps
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CC golynucleotide sequences. These are used in the method comprises treating a complement to sample with at least one LUIO5 specific nucleic acid. The method comprises treating a complement of the invention complement complement acid sequences (AAV54616 to AAV54621). LUIO5 is a lung disease marker. CC cells transformed with a recombinant expression system that contains complement complements are used to express recombinant contains complements. The antibodies are cused to express recombinant contains complements are used to express recombinant contains complements. The antibodies are used to detect the LUIO5 antigen, and correspondingly this antigen is complements, are used to express recombinant contains complements. The antibodies are used to detect the LUIO5 antigen, and correspondingly this antigen is considered to detect specific antibodies, in usual immunoassays. The LUIO5 considering, prognosis, prevention, treatment and determination of considering, prognosis, prevention, treatment and determination of concentration, in altered form or in an unusual body compartment). LUIO5 concentration, in altered form or in an unusual body compartment). LUIO5 can be detected in blood, plasma or serum in an inexpensive, non-invasive concentration.
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Best Local 9
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30-OCT-1998
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Granados EN, Hodges
Russell JC, Stroupe
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               30-JAN-1998;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           06-AUG-1998
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          New nucleic acid for the lung disease marker LU105 - polypeptides, antibodies and genes, used for diagnosis, prevention, treatment of lung disease, specifically cancer
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      WPI; 1998-437479/37
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        (ABBO ) ABBOTT LAB.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Claim 11; Fig 1; 123pp; English
                                                                                                                                                                                                                         Sequence 190 BP; 18
                                                                                                                                                                                                                                                     (Updated on 25-MAR-2003 to correct PI field.)
                                                                                                                                                                                Local
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   specific polynucleotide sequence from clone 3353867
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           lung disease marker; immunoassay; lung disease; cancer;
plasma; serum; ss.
                                                                                                          al Similarity
117; Conserv
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(first entry)
   121
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ges SC,
upe SD;
                                                                                                                                                                                                                            A; 69 C; 67 G;
                                                                                                                                                                                    21.2%;
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Klass MR, Kratochvil JD, Rob
                                                                                                                                                                        0;
                                                                                                                                                                                     Score 117; DB 19;
Pred. No. 4.3e-14;
                                                                                                                                                                          Mismatches
                                                                                                                                                                                                                                 32 T; 4 other;
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                                                                                                                                                                                                     Length 190;
                                                                                                                                                                             Indels
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ARZSULT 3
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                XX AAZ98109 to AAZ98242 encode AAX87224 to AAX87357 which represent the CC human signal peptide-containing proteins HSPP-1 to HSPP-134. HSPPs have anticancer, anti-inflammatory, antimicrobial, nootropic, hepatotropic, concerning or anti-inflammatory, antimicrobial, nootropic, hepatotropic, activities, and can gene therapy. HSPPs can be used to treat or prevent disorders associated with decreased activity or function of HSPP are associated with increased concerning of HSPP. Such diseases include cell proliferation concerning or the concerning of HSPP. Such diseases include cell proliferation of HSPP are used to treat or prevent disorders associated with increased concerning cancerning or HSPP. Such diseases include cell proliferation concerning or HSPP. Such diseases include cell proliferation concerning or HSPP. Such diseases include cell proliferation concerning or HSPP. Such diseases include cell proliferation or astable anticological proportion of HSPP. Antagonists and concerning or the concerning or the concerning or the concerning or the recombinant production of HSPP, for concepts and monitoring), in gene therapy, as antisense, large transfer or detecting HSPP in standard hybridisation and amplification assays (for concepts of the proportion of HSPP, for concepts of the proportion of HSPP, for concerning or ribozyme therapeutics, for detecting related sequences triplex-forming or ribozyme therapeutics, for detecting related sequences concerning the specific antibodies (Ab) and to screen for agonists and concepts and for chromosomal mapping. HSPP are also used to concepts the proportion of HSPP concerning or the proportion of HSPP concepts and proportion of HSP
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      26-JUN-1998;
31-JUL-1998;
01-OCT-1998;
11-DEC-1998;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           New human signal peptide-containing proteins useful in treatment, prevention and diagnosis of e.g. cancer, inflammation and cardiovascular disease
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Claim 9; Page 289; 327pp; English.
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DB; AAY87288.
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Au-Young J,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              98US-0090762.
98US-0094983.
98US-0102686.
98US-0112129.
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Yue
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Corley NC, Guegler KJ, Bi
H, Patterson C, Reddy R,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        CDNA SEQ
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R, Hillman
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Best Local
                                                                                                                                                                                                                                                                                                                                                               The present sequence is a lung specific gene (LSG) Lng107 from human clone ID S66271. The LSG has high level of tissue specificity for lungs and is overexpressed in cancerous tissues. The sequence serves as a diagnostic marker for detecting, monitoring, staging and prognosticating lung cancer. The diagnosis involves comparing levels of LSG in samples obtained from patient and normal control.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Claim 6;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       A new method for diagnosing, monitoring
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     WPI; 2000-116320/10.
P-PSDB; AAY44458.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Yang F,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Lung Specific Gene;
prognosticate; lung
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 AAZ29723 standard;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Sequence 543 BP; 89
                                                                                                                                                                                                                                                                                                                  Sequence 543 BP; 89 A; 194 C; 178 G; 82 T; 0 other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         21-мат-1998;
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                                                                                                                                                                                                          l Similarity
92; Conserv
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Similarity
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   CAGGTTCCCCGCGCGCGCCCCGAGCCCCCCGCGCC 551
                                                                                                                     CCGGCGCTGGAGGGCCGAGGACCGGGTATAAGAAGCCTCGTGGCCCTTGCCCGGGCAGCCG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Page 36; 40pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              CAGGTTCCCCGCGCGCGCCCGAGCCCCCGCGCC 551
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                                                                                                                                                                                                      Conservative
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Conservative
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93..407
/*tag= a
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            /*tag= a
/product= "LSG Lng107 protein"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    DNA;
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100.0%; Pr
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100.0%; Pr
100.0%; Pr
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      entry)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Sun
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        543
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Pred. No. 2.9e-09;
                                                                                                                                                                                                                             Score 92;
Pred. No.
                                                                                                                                                                                                      Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Mismatches
                                                                                                                                                                                                                             DB 21;
. 2.9e-09;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          and staging lung
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      T; 0 other;
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                                                                                                                                                                                                                                                          Length 543
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                                                                                                                                                                                                      Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              cancer
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                                                                                 RESULT 6
AAV54621
ID AAV5
AC CDS
FT CDS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      밁
                                                                                                                                                                                      Sequences shown in AAV54616 to AAV54621 represent LUIO5 specific
Copolynucleotide sequences. These are used in the method of the invention
Copolynucleotide sequences. These are used in the method of the invention
Copolynucleotide tuilo5 nucleic acid. The method comprises treating a
Copolynucleotide tuilo5 nucleic acid. The method comprises treating a
Copolynucleotide tuilo5 specific nucleic acid, or its complement
Copolynucleotides tuilo5 specific nucleic acid. Specific nucleic
Copolynucleotides (AAV54616 to AAV54621). LUIO5 is a lung disease marker.
Copolynucleotides (AAV54616 to AAV54621). LUIO5 is a lung disease marker.
Copolynucleotides which a recombinant expression system that contains
Copolynucleotides which are used to express recombinant
Copolynucleotides which are used to raise antibodies. The antibodies are
Copolynucleotides which are used to raise antibodies. The antibodies are
Copolynucleotides and nucleic acid sequences are used for diagnosis, staging,
Copolynucleotides are also used to screen for specific ally cancer. The LUIO5
Copolynucleotides are also used to screen for specific binding agents, useful
Copolynucleotides are also used to screen for lung disease (present at high
Copolynucleotides are also used to screen for lung disease (present at high
Copolynucleotides are also used form or in an unusual body compartment). LUIO5
Copolynucleotides are used form or in an unusual body compartment). LUIO5
Copolynucleotides are also used form or in an unusual body compartment). LUIO5
Copolynucleotides are used form or in an unusual body compartment). LUIO5
Copolynucleotides are used form or in an unusual body compartment). LUIO5
Copolynucleotides are used form or in an unusual body compartment). LUIO5
Copolynucleotides are used form or in an unusual body compartment). LUIO5
Copolynucleotides are used form or in an unusual body compartment.
Query Match
Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       New nucleic acid for the lung disease marker LU105 - polypeptides, antibodies and genes, used for diagnosis, prevention, treatment of lung disease, specifically cancer
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Billing-medel PA, Co
Granados EN, Hodges
Russell JC, Stroupe
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Claim 11; Fig 1; 123pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       31-JAN-1997;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     LU105; lung disease marker; blood; plasma; serum; ss.
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                                                                                    Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   P-PSDB;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             WPI;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            (ABBO ) ABBOTT LAB
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30-OCT-1998
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DB; AAW75868.
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                                                                                       519
                                                                                                                                            on 25-MAR-2003 to correct PI field.)
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(first entry)
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79..33
/*tag= a
/transl_except= (pos:136..138,
/product= "LU105 polypeptide"
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jes SC,
ipe SD;
                                                                                    A; 190 C; 170 G; 81
   14.2%;
100.0%;
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   Score 78;
Pred. No.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ВP
      DB 19;
1.5e-06;
                                                                                    T; 0 other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           aa:Val)
                                Length 519;
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Robertsrapp L;
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Ş 밁 δÃ

Matches

78;

Conservative

0;

474

밁 γQ Ъ δõ

534 61

GCCCGAGCCCCGCGCC 78
GCCCCGAGCCCCCGCGCC 78

Н

15-JUL-2002 ABK40267;

(first entry)

cDNA encoding human PRO1245

ABK40267 standard; cDNA; 569

ВР

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Human; PRO; benign tumour; malignant tumour; lymphoid malignancy; leukaemia; neuronal disorder; stromal disorder; blastocoelic disorder; inflammatory disorder; immune disorder; angiogenic disorder; gene therapy; cytostatic; neuroprotective; gene; ss.
The present invention relates to the isolation of novel human PRO polypeptides and the polynucleotide sequences encoding them. The PRO polypeptides, agonists, antagonists or anti-PRO antibodies are useful for treating benign or malignant tumours (e.g. renal, kidney, bladder, breast, etc), leukaemias and lymphoid malignancies, other disorders such as neuronal, glial, astrocytal, hypothalamic, glandular,
                                                                                                                            Thirty five nucleic acids encoding PRO polypeptides, useful for treating benign or malignant tumours, leukaemias and lymphoid malignancies, inflammatory, angiogenic and immunologic disorders
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             GCGAGGACCGGGTATAAGAAGCCTCGTGGCCTTGCCCGGGCAGCCGCAGGTTCCCCGCGC 533
                                                                                                                                                                                                                                             Goddard A, Godowski PJ,
Pan J, Pitti RM, Roy MA,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 polypeptide.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Mismatches
                                                                                                                                                                                                                                                    Gurney
Smith
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             0;
                                                                                                                                                                                                                                                     ۷, <sup>A</sup>L,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Indels
                                                                                                                                                                                                                                                     Hillan KJ;
Stone DM;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              0;
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                  02-JUN-1998;
02-JUN-1998;
02-JUN-1998;
03-JUN-1998;
04-JUN-1998;
05-JUN-1998;
05-JUN-1998;
05-JUN-1998;
10-JUN-1998;
11-JUN-1998;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Sequence 569 BP; 128 A; 190 C; 170 G; 81 T; 0 other;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Membrane-bound polypeptide; PRO polypeptide; LDL receptor; pharmaceutical; receptor immunoadhesin; gene mapping; ss.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Membrane-bound
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              05-APR-2000
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          02-JUN-1999;
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                    98US-0087607

98US-008759

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98US-0088028

98US-0088030

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98US-0088030

98US-0088202

98US-0088202

98US-0088212

98US-0088212

98US-0088717

98US-0088717

98US-0088774

98US-00888774

98US-00888774
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     protein PRO1245 encoding cDNA.
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; Pred. No.
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. 1.5e-06;
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RESULT 7
ABK40291
ID ABK4
XX ANA ABK4029
AC ABKX
XX CDN
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XX CDN
XX GEN
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99WO-US05028.
99US-123972P.
99US-133459P.
99US-140650P.
99US-140653P.
99US-14758P.
99US-145698P.
99US-145698P.
99US-151689P.
99US-151689P.
99WO-US280313.
99WO-US280313.
99WO-US280313.
99WO-US280313.

22-JUN-1999 22-JUN-1999 20-JUL-1999 26-JUL-1999 26-JUL-1999 28-JUL-1999 28-JUL-1999 31-AUG-1999 31-SEP-1999 31-SEP-1999 30-NOV-1999 01-DEC-1999 01-DEC-1999 01-DEC-1999

Ashkenazi AJ, Marsters SA, Watanabe CK,

Pan J, Wood WI;

2002-205567/26.

AAU86141.

(GETH) GENENTECH INC.

Claim

50; Fig 27; 302pp; English.

08-MAR-1999; 11-MAR-1999; 11-MAY-1999; 02-JUN-1999;

11-FEB-2000; 26-JUL-2001 WO200153486-A1 Homo sapiens.

2000WO-US03565.

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12-JUN 1998
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98U$-0089105.
98U$-0089440.
98U$-0089512.
98U$-00895314.
98U$-0089538.
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Best Local S
Matches 78
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18-AUG-1998
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26-AUG
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Wood WI,
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P-PSDB;
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DB; AAY66757.
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                      61
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Yuan
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98US -0096778
98US -00967791
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98US -0096959
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98US -0097951
98US -00977218
98US -00977218
98US -0097951
98US -0097977
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The invention provides membrane-bound PRO polypeptides and polynucleotides encoding them. The PRO sequences of the invention were identified based on extracellular domain homology screening. The PRO sequences have homology with proteins including LDL receptors, TIE ligands and various enzymes. The membrane-bound proteins and receptor immunoadhesins, for instance, can be used as therapeutic agents. Receptor receptor-ligand interactions. The membrane-bound proteins can also be employed for screening of potential peptide or small molecule inhibitors of the relevant receptor-ligand interaction. The PRO encoding sequences are useful as hybridization probes, in chromosome and gene mapping and in the generation of antisense RNA and DNA. PRO nucleic acid sequences will also be useful for the preparation of PRO polypeptides, especially by recombinant techniques.
                                                                                                                                                                                                                                                                      Sequence 570 BP; 129 A; 190 C; 170
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Claim 2; Fig 289; 822pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Membrane-bound proteins and related
                                                                                                                                                                           GCCCCGAGCCCCCGCGCC 551
                                                                                     Α,
                                                                                                                                                                                                   Score 78;
Pred. No.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Gurney AL,
                                                                                                                                                                                   Mismatches
                                                                                                                                                                                                                                                                      G; 81 T; 0 other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         nucleotide
                                                                                                                                                                                1.5e-06;
hes 0;
                                                                                                                                                                                                                               DB 21;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         sequences
                                                                                                                                                                                                                     Length 570;
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                                                                                                                                                                                Indels
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                                                                                                                                                                              0;
                                                                                                                                                                              Gaps
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23-JUN-1999;
23-JUN-1999;
07-JUL-1999;
26-JUL-1999;
26-JUL-1999;
28-JUL-1999;
17-AkG-1999;
17-AkG-1999;
18-SEP-1999;
16-DEC-1999;
01-DEC-1999;
01-DEC-1999;
16-DEC-1999;
16-DE
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                AAF44249 standard; cDNA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Human PRO1245 (UNQ629) nucleotide sequence
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Ferrara N, Fo
Grimaldi CJ,
Roy MA, Stewa
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      30-MAR-2000;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 07-DEC-2000
The present invention describes human secreted and transmembrane PRO proteins. The PRO proteins have cytostatic activity. The PRO proteins can be used for targeted delivery of bioactive molecules, such as expected solutions, radiolabels or antibodies, that cause cell death. PRO nucleotide sequences, and their fragments, can be used as hybridisation probes, in sequences, and gene mapping, and in the generation of anti-sense RRA and DNA. They may also be used to produce transgenic animals which are used to develop and screen therapeutically useful reagents. The PRO
                                                                                                                                                                                                                                                                                                                                                 WPI; 20
P-PSDB;
                                                                                                                                                                                                                                                   PRO polynucleotides used bloactive molecules such specific cells, to cause
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    (GETH )
                                                                                                                                                                                                              Claim
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                                                                                                                                                                                                                                                                                                                                                 2001-032160/04.
DB; AAB65280.
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                                                                                                                                                                                                           2; Fig
                                                                                                                                                                                                                                                                                                                                                                                                                                      zi AJ, Baker KP, Botstein D, Desnoyers L, Eaton
N, Fong S, Gerber H, Gerritsen ME, Goddard A,
i CJ, Gurney AL, Kljavin IJ, Napiter MA, Pan J,
Stewart TA, Tumas D, Watanabe CK, Williams PM,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       GENENTECH INC.
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99US-0141037

99US-0144758

99US-0146222

99US-0146222

99US-0146222

99US-0146222

99WO-US21090

99WO-US21090

99WO-US210313

99WO-US28301

99WO-US28301

99WO-US30951

2000WO-US00251

2000WO-US00251

2000WO-US00254

2000WO-US04314

2000WO-US0504414

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                                                                                                                                                                                                              289; 935pp; English.
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                                                                                                                                                                                                                                                        to produce polypeptides used to target as toxins, radiolabels or antibodies, targeted cell death -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ВÞ
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Godowski PJ;
Paoni NF;
Wood WI;
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                                RESULT 10
RABX80
ID ABX80
XX ABX80
AC ABX80
XX V 28-AE
XX Hummar
KW Cardd
KW Cardd
KW cardd
KW chon
XX Homo
XX Hom
XX 
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Best Local S
Matches 78
                             05-NOV-1997
16-SEP-1998
17-SEP-1998
07-OCT-1998
07-OCT-1998
05-JAN-1999
02-JUN-1999
15-SEP-1999
15-SEP-1999
15-SEP-1999
16-DEC-1999
01-DEC-1999
01-DEC-1999
16-DEC-1999
16-JAN-2000
11-FEB-2000
18-FEB-2000
24-FEB-2000
24-FEB-2000;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       19-SEP-2002
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Homo sapiens.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            14-NOV-2001;
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nucleotide and protein sequence can be used for tissue typing and in treating cancer. Anti-PRO antibodies can be used in diagnostic assays. ARF4470 to AAF44470 represent PCR primers and hybridisation probes used in the isolation of human PRO sequences. AAF44087 to AAF44269 and AAB65134 to AAB65300 represent human PRO polynucleotide and protein AAB6510 represent human PRO polynucleotide and protein sequences given in the exemplification of the present invention.
                                                                                                                                                                                                                              used
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Sequence 570 BP; 129 A; 190 C; 170 G; 81 T; 0 other; ch 14.2%; 1 Similarity 100.0%; 78; Conservative (Score 78; DB 22; Pred. No. 1.5e-06; 0; Mismatches Length 570; 0; Gaps 60 533

GCCCCGAGCCCCCGCGCCC 551

78

ABX80386 standard; secreted or transmembrane protein PRO1358 DNA. (first entry) DNA; 570

Human; PRO; hypertrophy of neonatal heart; anglogenesis; wound healing; cardiac insufficiency disorder, cancer; tumour; immune response; addrenal cortical capillary endothelial growth; c-fos induction; vascular endothelial growth factor inhibition; VEGF inhibition; endothelial growth inhibitor; T-lymphocytes stimulation; retinal cell growth inhibitor; Tod photoreceptor cell survival; rod photoreceptor cell survival; retinal disorder; retinitis pigmentosum; kidney disorder; memmallian kidney mesangial cell proliferation; Berger disease; dermatitis; herperiformis; Crohn's disease; chondrocyte proliferation; chondrocyte redifferentiation; sports injury; arthritis; gene; ds.

US2002132252-A1.

98WO-US19330 98WO-US19437. 98WO-US21141. 98WO-US251108. 99WO-US05108. 99WO-US05028. 99WO-US12252. 99WO-US21090. 99WO-US213090. 99WO-US283131. 99WO-US28313. 2001US-0990442.

2000WO-US05841. 2000WO-US06319. 2000WO-US06884. 2000WO-US07377.

Paoni Wood DL; Godowski

WI;

PJ;

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RESULT 11
ABX80890
ID ABX80
XX
AC ABX80
XY
DT 22-AP
XX
DE Human
XX
Human
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                                                                                                                                                                                                                                                                                                                                                                                                                     δÃ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     The invention describes an isolated human PRO polypeptide. The PRO CC polypeptides are useful in detecting PRO polypeptides in a sample, in CC linking a bioactive molecule to a cell expressing a PRO polypeptide, and CC in modulating at least one biological activity of a cell expressing a PRO CC polypeptide. PRO1312 stimulates hypertrophy of neonatal heart and is thus CC useful for treating cardiac insufficiency disorders. PRO1154 and PRO1366 CC pRO1369 and PRO1387 induce c-fos in endothelial growth, and PRO536, CC PRO1360 and PRO1387 induce c-fos in endothelial growth, and PRO536, CC pRO1360 and PRO1387 induce c-fos in endothelial growth, and PRO536, CC pRO1360 and PRO1387 induce c-fos in endothelial cells, and are thus cells in the properties of this polypeptide are useful for treating conditions or disorders where angiogenesis would be beneficial, e.g. wound healing and ancagonist of this polypeptide are cells and is thus useful for inhibiting endothelial cell growth in cells and is thus useful for inhibiting endothelial cell growth in CC enls and is thus useful for inhibiting endothelial cell growth PRO826, CC pRO1068, PRO1184, PRO1346 and PRO1375 stimulated proliferation of endothelial cell growth in the proliferation of college proliferation of mammalian kidney mesangial cells, and therefore are useful for treating kidney disorders associated with dermatitis, herpetiformis or Crohin's college proliferation and/or redifferentiation of chondrocytes in culture and college proliferation and/or redifferentiation of chondrocytes in culture and college proliferation and college proliferation and arthritis. This sequence represents a novel human PRO protein polynucleotide.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Query Match
Best Local :
                                           Human secreted/transmembrane protein cDNA, #163.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Ashkenazi AJ, Baker KP, Botstein D, Desnoyers L, Eaton Ferrara N, Fong S, Gerber H, Gerritsen ME, Goddard A, Grimaldi JC, Gurney AL, Kljavin IJ, Napier MA, Pan J, Roy MA, Stewart TA, Tumas D, Watanabe CK, Williams PM, Zhang Z;
Human; gene; ss; PRO; secreted; transmembrane; pharmaceutical;
                                                                                      22-APR-2003
                                                                                                                                 ABX80890;
                                                                                                                                                                              ABX80890 standard; cDNA; 570
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Sequence 570
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 WPI; 2003-247083/24.
P-PSDB; ABU59174.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                     78;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                14.2%; Score 78; DB ilarity 100.0%; Pred. No. 1. Conservative 0; Mismatches
                                                                                      (first entry)
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. 1.5e-06;
ches 0;
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Indels

0;

Gaps

60

102-MAR 2000
15-MAR 2000
15-MAR 2000
15-MAR 2000
20-MAR 2000
17-MAR 1998
17-MAR 1998
17-MAR 1998
11-JUN 1998

2000WO-US21524 2000WO-US220710 2000WO-US233522 2000WO-US23522 2000WO-US23522 2000WO-US23522 2000WO-US2166 2001WO-US2166 2001WO-US21735 97US-0649789 98US-06511EP 98US-084600P 98US-088025P 98US-088025P 98US-088025P 98US-088212P 98US-089254P

(GETH) GENENTECH INC

ene therapy; tumour associated antigenic target; TAY; como sapiens. 16-FEB-2003. 16-FEB-2003. 15-NOV-2001; 2001US-0997428.	All. 2001US-0997428. 98WO-US19437. 98WO-US21141. 98WO-US21141. 98WO-US21141. 99WO-US25108. 99WO-US21090. 99WO-US21090. 99WO-US21090. 99WO-US21090. 99WO-US21090. 99WO-US21090. 99WO-US21091. 2000WO-US203011. 2000WO-US203011. 2000WO-US203011. 2000WO-US20311. 2000WO-US20314. 2000WO-US20314. 2000WO-US20314. 2000WO-US20314. 2000WO-US20314. 2000WO-US20314. 2000WO-US20314. 2000WO-US2031. 2000WO-US200. 2			ס מים אים מים מים מים מים מים מים מים מים מים מ			0.10
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therapy;	therapy;	98US-084302P 98US-084600P 98US-087106P 98US-087607P 98US-087607P 98US-087759P 98US-088021P 98US-088021P	2001WO-US21706. 2001WO-US217735. 97US-0497879. 97US-0651869. 97US-0651119. 97US-0653119. 98US-0759459. 98US-0779451.	2000WO-US08439 2000WO-US13358 2000WO-US13705 2000WO-US14941 2000WO-US15264 2000WO-US20710 2000WO-US220711 2000WO-US23522 2000WO-US23522 2000WO-US23328 2000WO-US33678 2000WO-US36520 2001WO-US16520 2001WO-US17800	99WO-US28313 99WO-US28331 99WO-US28634 99WO-US30095 99WO-US30091 99WO-US30091 2000WO-US00219 2000WO-US03565 2000WO-US03564 2000WO-US04914 2000WO-US04914 2000WO-US05841 2000WO-US05841 2000WO-US05841 2000WO-US05841 2000WO-US05841 2000WO-US05841 2000WO-US05841 2000WO-US05841	2001US-0997428. 97WO-US20069. 98WO-US19330. 98WO-US119437. 98WO-US21141. 98WO-US25108. 99WO-US00106. 99WO-US05028. 99WO-US12252. 99WO-US12252.	; tumour-associate endent enzyme media -Al.
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RESULT 12
ABX81273
ID ABX81
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AC ABX81
XX
AC ABX81
XX
DT 22-AF
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DE NOVel
XX
Human
KW Cardi
KW adren
KW adren
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                       Human; PF
cardiac i
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20 AU
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                                                                                                                                                                                                                                                                                 ABX81273;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Match 14.2%;
Local Similarity 100.0%;
Local Similarity (100.0%;
Local 
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         474
                                                                                                                                                               human
         PRO; hypertrophy of neonatal heart; anglogenesis; wound he cinsufficiency disorder; cancer; tumour; famune response; contical capillary endothelial growth; c-fos induction; ar endothelial growth factor inhibition; VEGF inhibition;
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                                                                                                                                                                                                                                                                                                                                      standard;
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                                                                                                                                                                                                                 (first entry)
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98US-096143P

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98US-096894P

98US-096894P

98US-096897P

98US-096897P

98US-096897P

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98US-097972P

98US-097972P

98US-097971P

98US-097971P
                                                                                                                                                                                                                                                                                                                                   DNA;
                                                                                                                                                            Or.
                                                                                                                                                            transmembrane
                                                                                                                                                                                                                                                                                                                                      570
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                                                                                                                                                                                                                                                                                                                                      BP
                                                                                                                                                         protein PRO1358
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    DB 25; 1
1.5e-06;
hes 0;
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17-SEP-1998
07-OCT-1998
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98WO-US25106.
99WO-US25106.
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99WO-US28313.
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2000WO-US00376.
2000WO-US004341.
2000WO-US04441.
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2000WO-US1346.
2000WO-US1464.
2000WO-US1464.
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2000WO-US13780.
2001WO-US1567.
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2001WO-US1780.
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2001WO-US1780.
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2000WO-US1
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B 64 B 65

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RESULT 13
ABX9033
ID ABX90
AC ABX90
AC ABX90
XX 01-MA
XX U1-MA
XX Human
XX Human
XX Human
XX Homo
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30-JUL-1998;

04-AUG-1998;

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                                                                                         Human; gene; ss;
pharmaceutical; or
                                                                                                                                               Human secreted/transmembrane protein cDNA, #163.
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Ashkenazi AJ, Baker KP, Botstein D, Desnoyers L, Eaton Ferrara N, Fong S, Gerber H, Gerritsen ME, Goddard A, Grimaldi JC, Gurney AL, Kljavin IJ, Napier MA, Pan J, Roy MA, Stewart TA, Tumas D, Watanabe CK, Williams PM, Zhang Z; Godowski PJ; Paoni NF; Wood WI;

WPI; 2003-288106/28. P-PSDB; ABU60604.

New transmembrane polypeptides and nucleic acids encoding the polypeptides, useful in gene therapy, in chromosome identification, chromosome markers, or in generating probes -

Claim 2; Fig 289; 650pp; English.

The invention discloses isolated PRO secreted/transmembrane polypeptides CC comprising a sequence without signal peptide and the nucleic acid CC encoding them. The polypeptides can be used to raise antibodies that CC specifically bind to the PRO polypeptide, for linking a bloactive molecule to a cell expressing a PRO protein and for modulating at least CC one biological activity of a cell. The PRO polypeptides or polynucleotides are also useful in gene therapy, in chromosome CC identification, as chromosome markers, or in generating probes. The PRO CC plypeptides are useful as molecular markers for protein CC electrophoresis, and the isolated nucleic acids may be used for cc electrophoresis, and the isolated nucleic acids may be used for cc acids may also be used in tissue typing. Anti-PRO antibodies are useful in diagnostic assays for PRO, and in affinity purification of PRO from CC acids may also be used in tissue typing. Anti-PRO antibodies are useful CC in diagnostic assays for PRO, and in affinity purification of PRO from CC ABX90083 ABX90468 are the genes encoding, the primers amplifying and the CC wrobes detecting the PRO polypucleotides of the invention. CC Note: The sequence data for this patent is also available in electronic format from USPTO at sequance sprey/sequence.)

Sequence 570 BP; 129 A; 190 C; 170 G; 81 T; 0 other;

Вþ Qy Query Match Best Local S Matches 78 ch 14.2%; Score 78; DB 25; I I Similarity 100.0%; Pred. No. 1.5e-06; 78; Conservative 0; Mismatches 0; Н GCGAGGACCGGGTATAAGAAGCCTCGTGGCCTTGCCCGGGGCAGCCGCAGGTTCCCCGCGC Length Indels 570; 0; 60 0

DEST/1974 Standard CDNA; 570 BP. ARX/7974; ARX ARX/7974; A	Db 61 GCCCGAGCCCCGCGCC 78 RESULT 14
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99W0-USS8634

99W0-USS03911

2000W0-USS03565

2000W0-USS03565

2000W0-USS03441

2000W0-USS0441

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(GETH GENENTECH INC.

Zhang Ashkenazi AJ, Baker KP, Botstein D, Desnoyers L, Eaton Ferrara N, Fong S, Gerber H, Gerritsen ME, Goddard A, Grimaldi JC, Gurney AL, Kljavin IJ, Napier MA, Pan J, Roy MA, Stewart TA, Tumas D, Watanabe CK, Williams PM, 2; Godowski Godowski Paoni NF: Wood WI WI; PJ;

P-PSDB; 2003-155950/15. DB; ABU59026.

New secreted and transmembrane PRO polypeptides (e.g. PRO183, PRO184, PRO361 or PRO846) useful as targets for therapeutic intervention in cancers (e.g. lung or breast cancers), or for diagnosing these cancer: cancers

Claim Fig 289; 647pp; English.

The invention discloses isolated PRO secreted/transmembrane polypeptides comprising a sequence without signal peptide and the nucleic acid encoding them. The polypeptides can be used to raise antibodies that specifically bind to the PRO polypeptide, for linking a bioactive molecule to a cell expressing a PRO protein and for modulating at least one biological activity of a cell. The PRO polypeptides or polynucleotides are also useful as pharmaceuticals, diagnostics, biosensors or bioreactors, for detecting or treating e.g. tumours in mammals, e.g. humans, dogs, cats, cattle, horses, sheep, pigs, goats or rabbits as targets for therapeutic intervention in certain cancers (e.g. colon, lung or breast cancers) and diagnostic determination of the presence of these cancers. The PRO polypeptides are also useful as molecular weight markers or for chromosome identification. The PRO genes

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                                                                                                                                                                                                  are useful as hybridisation probes or for screening libraries of hum cDNA, genomic DNA or mRNA. The PRO genes may also be used in gene therapy, particularly for replacing a defective gene. The sequences presented in ABX79290-ABX79675 are the genes encoding, the primers amplifyling and the probes detecting the PRO polynucleotides of the invention.

Note: The sequence data for this nateral in the PRO polynucleotides of the content of the sequence data for this nateral invention.
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                                                  534 GCCCCGAGCCCCCGCGCC
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                                Contact: Genoscope
Genoscope - Centre National de Sequencage
Bp 191 9106 EVRY cedex - France
Bp 191 9106 EVRY cedex - France
Email: seqref@genoscope.cns.fr, Web: www.genoscope.cns.fr
Library was constructed by Life Technologies, a division of
Library was constructed by Life Technologies, a division of
Invitrogen. Contact: Feng Liang Email: fliang@lifetech.com URL
http://fulllength.invitrogen.com/ InVitroGen Corporation 1600
Faraday Avenue Genoscope sequence ID: CSOCAPO04BE10QP1.
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Li,W.B., Gruber,C., Jessee,J. and Polayes,D. Full-length cDNA libraries and normalization unpublished
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Drosophila melanogaster (fruit fly)
Drosophila melanogaster
Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
Neoptera; Endoptera; Diptera; Brachycera; Muscomorpha;
Ephydroidea; Drosophilidae; Drosophila.

(bases 1 to 935)
Genoscope.

Direct Submission

Submitted (02-yUN-1999) Genoscope - Centre National de Sequencage :

BP 191 91006 EVRY cedex - FRANCE (E-mail : seqref@genoscope.cns.fr - Web : www.genoscope.cns.fr)

Determination of this BAC-end sequence was carried out as part of a collaboration with the Berkeley Drosophila Genome Project (BDGP). The BDGP is constructing a physical map of the Drosophila
                                                                                                                                                                                              DNA linear GSS 03-JUN-1999 Drosophila melanogaster genome survey sequence T7 end of BAC # BACR14N09 of RPCI-98 library from Drosophila melanogaster (fruit fly), genomic survey sequence.
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Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vert
Mammalla; Eutherla; Primates; Catarrhini; Ho
1 (bases 1 to 982)
Li,W.B. Gruber(C. Jessee, J. and Polayes, D.
Full-length cDNA libraries and normalization

Craniata; Vertebrata; Euteleostomi; Catarrhini; Hominidae; Homo.

Homo sapiens (human)

COMMENT

Unpublished Contact: Ger

Genoscope

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           melanogaster genome using these BACs. For further information please see http://www.fruitfly.org The BDGP Drosophila melanogaster BAC library was prepared by Kazutoyo Osoegawa and Aaron Mammoser in Pieter de Jong's laboratory in the Department of Cancer Genetics at the Roswell Park Cancer Institute in Buffalo, NY. The library is named RPCI-98 and was constructed by partial EcoRI digestion of Drosophila DNA provided by the BDGP from the Isogenic strain 92; cn bw sp. the same strain used for the BDGP's pl and EST libraries. A more detailed description of the library and how to order individual BAC clones, the entire library, or filters for hybridization from the BACPAC Resource Center can be found at http://bacpac.med.buffalo.edu/drosophila_bac.htm.
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5-PRIME, mRNA sequence.
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/note="end : T7"
/note="foot : T7"
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Pred. No. 1.46
2; Mismatches
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CS0CAP004YI20
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RESULT 4
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145; Conserv
                                                                                                                           CRS015Y4 1203 bp DNA linear GSS 26-JUL-1999 Drosophila melanogaster genome survey sequence T7 end of BAC BACN15E10 of DrosBAC library from Drosophila melanogaster (fruit fly), genomic survey sequence.

AL106054.1 GI:5619805
Drosophila melanogaster (fruit fly)
Drosophila melanogaster
Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
Neoptera; Endopterygota; Dlptera; Brachycera; Muscomorpha;
                                                                                                               SSD
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BP 191 91006 EVRY cedex - France
Email: seqref@enoscope.cns.fr, Web: www.genoscope.cns.fr
Library was constructed by Life Technologies, a division of
Invitrogen. Contact : Feng Liang Email: flang@lifetech.com URL
http://fulllength.invitrogen.com/ InvitroGen Corporation 1600
Faraday Avenue Genoscope sequence ID: CSOCAP004BE10QP1.
Location/Qualifiers
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Pred. No. 1.5e-05;
7; Mismatches 202;
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Best Local S
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175; Conserv
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Submisted (23-JUL-1999) Genoscope - Centre National de Sequencage :

Submitted (23-JUL-1999) Genoscope - Centre National de Sequencage :

BP 191 91006 EVRY cedex - FRANCE (E-mail : segref@genoscope.cns.fr)

Web : www.genoscope.cns.fr)

Determination of this BAC-end sequence was carried out as part of a collaboration with the European Drosophila Genome Project (EDGP) - http://www.edgp.ebl.ac.uk - This Drosophila melanogaster BAC library (Dros BAC) was made by Alain Billaud at CEPH (Centre d'Etude du Polymorphisme Humain) with funding provided by a MRC project grant. The DNA was prepared from embryos by Alain Bucheton and Genevieve Payan. It has been constructed in the vector pBeloBAC11.
           AG032885
Pan troglodytes DNA,
AG032885
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1 (bases 1 to 1203)
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/note="84 c 380 g 158 t 237 ot
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                                 1313 bp DNA clone: PTB-007M05.F,
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Pred.
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NO. 6.6e-05;
Mismatches 224.
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3 (bases 1 to 1313)
4 (bases 1 to 1313)
5 (bases 1 to 1313)
7 (bases 1 to 1313)
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8 (bas
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Eukaryota; Mețazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Pan.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Pan troglodytes (chimpanzee)
Pan troglodytes
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    AG032885.1 G1:16559758
GSS.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                          AGTGCCCGACGTTGCCACGGTCTGGGATCAGAGGCAGGGACCAGGGAACTGCG 146
                                          GCCGCAGCAGGAAGTTGGCCAGGGCACGGCCGTGAGCGGAGCGGGCAGGGCTTTCTCAGG 446
                                                                                                                                                                    GCGCGGGCAAGGGGGGTTANGGNGCGCGCGCGGGGGCGGNCGGCNCCGGNGCCGGG
                                                                                                                                                                                                                                                             CCCGGCCCAGCCCTGCAGGGGGGGGGCGTGGGGTCAGACCGCAAAGCGAAGGTGCGGGCCG
                                                                                                                                                                                                                                                                                                                                             CGGNCGGCGGNGCGGCGNGCGGNCGCGNGCGCACACGGCGNGGGAAGGCCGG
                                                                                         CAAGAGGAAGTCCTCGAGGCCCGGGCAGGGAAGGGGGCACGGGCTTCCCAGGGCCCGCCG
                                                                                                                                                                                                    GGGTGGGCCTCG¢GGAGACAAAGGCCGGGCCTGCCTCTCAGAGGGCCCAGCGCCTGC
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R.Site 1 : SacI
R.Site 2 : SacI.
Location/Qualifiers
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/clone_lib="PTB Chimpanzee Male
389 c 502 g 132 t 2
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/mol_type="genomic DNA"
/db_xref="taxon:9598"
/clone="PTB-007M05.F"
/sex="male"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            43.48;
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Pred. No. 6.6e-05;
Mismatches 296;
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225 others
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ORIGIN
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CNS0091P/c
LOCUS
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Best Local
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Determination of this BAC-end sequence was carried out as part of a collaboration with the Berkeley Drosophila Genome Project (BDGP). The BDGP is constructing a physical map of the Drosophila melanogaster genome using these BACs. For further information please see http://www.fruitfly.org The BDGP Drosophila melanogaster BAC library was prepared by Kazutoyo Osoegawa and Aaron Mammoser in Pleter de Jong's laboratory in the Department of Cancer Genetics at the Roswell Park Cancer Institute in Buffalo, NY. The library is named RPCI-98 and was constructed by partial ECORI digestion of Drosophila DNA provided by the BDGP from the isogenic strain y2; on bw sp, the same strain used for the BDGP's and was constructed by the Ibrary and how to order individual BAC clones, the entire library, or filters for hybridization from the BACPAC Resource Center can be tronger for hybridization buffalo.edu/drosophila_bac.htm.
                                                                                                                                                                                                     298
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                                                358
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48; Conserv
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Drosophila melanogaster
Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
Ephydroidea; Drosophilidae; Drosophila.
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Drosophila melanogaster genome sur
BACR19D16 of RPCI-98 library from
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Genoscope.
Direct Submission
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CVKCNASSSCGCCGCGMABCCMCSSSSSCCGSASARGVKVRASGGAGKRGGGSGGASASH
                                                                                                                  GTCAGACCGCAAAGCGAAGGTGCGGGCCCGGGGTGGGCCTCGCGGAGACAAAGGCCGGGCC
                                                                                                                                                                                                                                                                                                                                                                                                                   TGCCTCTCTCAGAGGGCCCCAGCGCCTGCCAAGAGGAAGTCCTCGAGGCCCGGGCAGGGA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        /organism="brosophila melanogaster"
/mol_type="genomic DNA"
/db_xref="faxon:7227"
/clone="BACR19D16"
/clone_lib="RBCI-98"
/note="end: TEI3"
/note="end: TEI3
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survey sequence TET3 end of BAC #
rom Drosophila melanogaster (fruit
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AUTHORS
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SOURCE
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VERSION
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ORIGIN
                                                                                                                       Query Match
Best Local Similarity
Matches 250; Conserv
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Contact: Charles Hauser DCMB Box 91000
Duke University
Durham, NC 27708-1000
Tel: 919 613 8159
Fax: 919 613 8177
Email: chauser@duke.edu
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1281 bp mRNA linear EST 29-MAY-20/
1024034A03.y2 C. reinhardtii CC-1690, normalized, Lambda Zap II
Chlamydomonas reinhardtii CDNA, mRNA sequence.
BG852363.1 GI:14233547
EST.
Chlamydomonas reinhardtii
Chlamydomonas reinhardtii
Eukaryota; Viridiplantae; Chlorophyta; Chlorophyceae; Volvocales;
Chlamydomonadaceae; Chlamydomonas.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Grossman, A., Davies, J., Federspiel, N., Harris, E., Lefebvre, P., McDermott, J.P., Silflow, C., Stern, D., N. and Surzyck, R. McDermott, J.P., Chlamydomonas reinhardtii Genome: A Model, Analyses of the Chlamydomonas reinhardtii Genome: A Model, Unicellular System for Analyzing Gene Function and Regulation Vascular Plants; project phase 2
Unpublished
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                                                                                                                       14.0%;
ilarity 45.8%;
Conservative
                                                                                                                                                                                                                                                        30
                                                                                                                                                                                                                                            /note="Vector: pBluescript II SK-; Site_1: EcoRI; Site_2: XhOI; This library, constructed by John Davies and Jeffrey XhOI; This library, constructed by John Davies and Jeffrey McDermott, combines coNAs from CC-1690 cells grown to mid-log phase in TAP (acetate-containing) medium in the light. TAP medium in the dark, HS (minimal) medium in ambient levels of CO2 and HS medium bubbled with 5% CO2. PolyA mRNA was purified from each sample, pooled and cDNA synthesized. The cDNA was directionally cloned into lambda SAP II (Stratagene) in the EcoRI (5') and XhOI (3') sites. PBluescript II SK- plasmids were excised from the lambda ZAP clones by superinfection with ExAssist (Stratagene) phage. The library was normalized using method 4 described in Bonaldo et al (1996) Genome Research 6: 791-806."
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     /organism="Chlamydomonas reinhardtii"
/mol_type="mRNA,"
/strain="CC-1690 wild type mt+ 21gr"
/db_xref="taxon:3055"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                /clone_lib="C. reinhardtii CC-1690, normalized, Lambda Zap
                                                                                                                    Score 77.2; DB 12;
pred. No. 7.8e-05;
0; Mismatches 294;
                                                                                                                              Indels
                                                                                                                                                                            Length 1281;
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Lambda Zap II
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                  Direct Submission

Direct Submission

Submitted (02-JUN 1999) Genoscope - Centre National de Sequencage :

But 191 191006 EVRY cedex - FRANCE (E-mail : seqref@genoscope.cns.fr - Web : www.genoscope.cns.fr)

Petermination of this BAC-end sequence was carried out as part of a collaboration with the Berkeley Drosophila Genome Project (BDGP). The BDGP is constructing a physical map of the Drosophila melanogaster genome using these BACs. For further information please see http://www.fruitfly.org The BDGP Drosophila melanogaster BAC library was prepared by Kazutoyo Oscegawa and Aaron Mammoser in Pieter de Jong's laboratory in the Department of Cancer Genetics at the Roswell Park Cancer Institute in Buffalo, NY. The library is named RPCI-98 and was constructed by partial EcorI digestion of Drosophila DNA provided by the BDGP from the isogenic strain y2; on bw sp, the same strain used for the BDGP's pl and EST libraries. A more detailed description of the library and how to order individual BAC clones, the entire library, or filters for hybridization from the BACPAC Resource Center can be
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Drosophila melanogaster genome BACR14B09 of RPCI-98 library fifly), genomic survey sequence.
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Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
Neoptera; Drosophilidae; Drosophila.
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 Fujiyama, A., Hattori, M., Toyoda, A., Totoki, Y., Watanabe, H. and Sakaki, Y. Direct Submission Submitted (02-AUG-2001) Asao Fujiyam and Chemical Research (RIKEN), Genom
                                                                           Fujiyama, A., Hattori, M., To
Totoki, Y., Watanabe, H. and
                                                                                                 Pan troglodytes (chimpanzee)
Pan troglodytes
Eukaryota, Metazoa; Chordata, Craniata, Vertebrata, Euteleostomi,
Mammalia; Eutheria; Primates, Catarrhini, Hominidae, Pan.
                                                                                                                                                AG043499 949 bp DNA
Pan troglodytes DNA, clone: PTB-021N08.F,
AG043349
AG043499.1 GI:16572224
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/organism="Drosophila melanogaster"

/mol_type="genomic DNA"

/mol_type="genomic DNA"

/db_xref="taxon:7227"

/clone="BACR14809"

/clone="lb-"RPCI-98"

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AGENCOURT_8187867 NIH_MGC_112 Homo
5', mRNA sequence.
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BO681076.1 GI:21793755
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               1-7-22 Suehiro-chou Tsurumi-ku, Yokohama, Kanagawa 230-0045, Japan (E-mail:chimpbes@gsc.riken.go.jp, URL:http://hgp.gsc.riken.go.jp/, Tel:81-45-503-9111, Fax:81-45-503-9170) Clones are derived from the chimpanzee BAC library PTB This BAC envas generated during the R&D process and may have higher chance of netwers.
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/clone_lib="PTB Chimpanzee Male BAC Library"
465 c 281 g 35 t 113 others
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/mol_type="genomic DNA"
/db_xref="taxon:9598"
/clone="pTB-021N08.F"
/sex="male"
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Pred. No. 0.000
0; Mismatches
                                                                                                                         351
                                                                                                                                                  550
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         DB 29;
.00036;
es 267;
                                               mRNA
sapiens
                                               linear EST 15-JUL-2002 CDNA clone IMAGE:6259803
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Length
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: :::	Qy 422 GCGGAGCGGGCAGGGCTTCTCAGGAGGGCGAGGCCGGGGGGGG
261	
Dh 815 CSAVSA	
755	600 GCGCCGGGGGCGGGCCGGCNGCGGGGGGGGGGGGGGG
Qy 246 GCAAAG	QY 302 TCTCTCAGAGGGCCCCAGCGCCTGCCAAGAGGAAGTCCTCGAGGCCCGGGCAGGGAAGGG 361
Db 695 ASCACM	Qy 242 GACCGCAAAGCCGAGGTGCGGGTGGGCCTGCCGGAGACAAAGGCCGGGCCTGCC 301
126	0y 182 CCTCACCNGAGGGAAGCTCCCCTCACCCGGCCCAGCCCTGCAGGGGGGGG
Matches 68; Cons	Db 780 GGGCCGCGGGGGGGCGGGGCCGCCCCCCNNNNCCGGCCGGGCGGGGGG
	ייי כנו
BASE COUNT 254 a	Qy 62 GCAGAAGGCGCCCACGAGGACCCCCAGTGCCCCACGTCTGCGATCAGAGGC 121 Qy 62 GCAGAAGGCGCCACGACGACGCCCCCAGTGCCCCAGCTGCACGCGCGCG
source	Query Match 45.6%; Prod. No. 0.00036; Best Local Similarity 45.6%; Prod. No. 0.00036; Prod. No. 0
	13.49:
project g and Genev	NIH_MGC Library." BASE COUNT 63 a 593 c 314 g 55 t 40 others ORIGIN
library (Berkeley) using ZAP-CDNA synthesis kit (Stratagene) and Superscript II RT (Life Technologies). Note: this is a
	GGCACGAG(G). Library constructed by Ling Hong in the laboratory of Gerald M. Rubin (University of California,
	<pre>ECORI; cDNA made by oligo-dT priming. Directionally cloned into EcoRI/XhoI sites using the following 5' adaptor:</pre>
JOURNAL Submitted	<pre>/clone_lib="NIH_MGC_112" /note="Organ: skin; Vector: pOTB7; Site_1: xhoI; Site_2:</pre>
Gen	<pre>/tissue_type="melanotic melanoma, cell line" /lab_host="DH10B (phage-resistant)"</pre>
Ephydroid Ephydroid 1 (bases	/db_xref="taxon:9606" /clone="IMAGE:6259803"
OKGANISM DIOSOPHIA: Eukaryota Neontera:	
Š	FEATURES Location/Qualifiers
ACCESSION ALIU8460 VERSION AL108460. KEYWORDS GSS.	Plate: LLCM2417 row: o column: 04 High quality sequence stop: 315.
	found through the I.M.A.G.E. Consortium/LINL at:
LOCUS CNS017SY DEFINITION Drosophile	cDNA Library Arrayed by: "The I.M.A.G.E. CONSOLUTION DNA Sequencing by: Agencourt Bioscience Corporation Clone distribution: MGC clone distribution information can be
RESULT 11	Tissue Procurement: DCTD/DTP CDNA Library Preparation: Rubin Laboratory
Db 362 GGCGGGCG	JOURNAL Unpublished COMMENT Contact: Robert Strausberg, Ph.D. COMMENT Comphs-remail nih.gov
Qy 542 CCCCCGCC	AUTHORS NIH-MGC http://mgc.nci.nin.gov/. TITLE National Institutes of Health, Mammalian Gene Collection (MGC)
pb 422 gegegec	Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo. REFERENCE 1 (bases 1 to 1065)
Qy 482 CGGGTATA	NISM Homo Euka
Db 482 CCGGCCCG	SOURCE Homo sapiens (human)

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/clone="apaCu37L08"
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/note="end : SP6"
1 a 176 c 160 g 152 t 359 otl
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la melanogaster
a; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
B; Endopterygota; Diptera; B; Bachycera; Muscomorpha;
B; Endopterygota; Drosophila.
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18 of DrosBAC library from Drosophila melanogaster (fruit nomic survey sequence.
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BASE COUNT
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AUTHORS
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ORGANISM
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                                                                                                                                                                                            Query Match
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Matches 256;
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                                                                          67 AGGCGCCCACGAGGACCCCCAGTGCCCACGGTTGCCACGGTCTGGGATCAGAGGCAGGGA 126
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4400 Fifth Avenue, Pittsburgh, P
Tel: +1 412 268 5849
Email: ettensohn@andrew.cmu.edu.
Location/Qualifiers
1. .1040
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Dept. Biol. Sci.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    A large scale analysis of mRNAs expressed by cells of the sea urchin embryo Development 128 (13), 2615-2627 (2001)
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BG786331
BG786331.1
          CCAGGGAGCCAGGAACTGCGCCGCCCCCCCCCCTGGCGGGGGAAGCTCCCTCA 186
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,X., Mahairas,G., Illies,M.R., Cameron,R.A., Davidson,E.H. and
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                                                                                                                                                                                                                                                library"
//note="Vector: pSPORT1; Site_1: Not1; Site_2: Sal1;
dt priming from poly A+ RNA, directionally cloned"
a 499 c 472 g 44 t 5 others
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                                                                                                                                                                                                                                                                                                                      /clone_lib="Sea urchin primary mesenchyme cell cDNA
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                                                                                                                                                                                                      13.38;
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Pred. No. 0.00042;
0; Mismatches 285;
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                                                                                                                                                                                                     Genoscope Centre National de Sequencage
BP 191 91006 EVRY cedex - France
Email: segref@genoscope.cns.fr, Web: www.genoscope.cns.fr
Library was constructed by Life Technologies, a division of
Invitrogen. This sequence belongs to sequence cluster 10245.r For
more information about this cluster, see
http://www.genoscope.cns.fr/
cgi-bin/cluster.gel7seg-C90AG006BD03NP1&cluster=10245.r. Contact
http://fulllength.invitrogen.com/ InvitroGen Corporation 1600
Faraddy Avenue Genoscope sequence ID : CSOAG006BD03NP1.
Location/Qualifiers
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1 (bases 1 to 1201)

11.W.B., Gruber,C., Jessee,J. and Polayes,D.

Full-length cDNA libraries and normalization

Contact: Genoscope
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             BX405071 1201 bp mRNA linear i
BX405071 Homo sapiens B CELLS (RAMOS CELL LINE) Homo
clone CSODG006YG06 3-PRIME, mRNA sequence.
BX405071
BX405071.1 GI:30648111
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Library was not normalized."
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546 394 486 453 426 513 366 573 306 633 246

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Library"

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Gaps

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692

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TITLE
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Best Local Similarity 35.4
Matches 196; Conservative
                                                                 AUTHORS
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Pan trogl
2 (bases 1 to 1085)
2 (bases 1 to 1085)
2 (bases 1 to 1085)
3 (bases 1 to 1085)
4 (bases 2 to 1085)
5 (bases 3 to 1085)
7 (bases 4 to 1085)
8 (bases 4 to 1085)
9 (bases 5 to 1085)
1-7-22 Suehiro-chou, Tsurumi-ku, Yokohama, Kanagawa 230-0045, Japan (B-mail:chimpbes@gsc.riken.go.jp, URL:http://hgp.gsc.riken.go.jp/,
                                                                                                                                sequence.
AG152796
AG152796
AG152797
AG152797
AG152797
GSS.
Pan troglodytes (chimpanzee)
Pan troglodytes
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Eukaryota; Metazoa; Chordata; Catarrhini; Hominidae;
                                                                                             Fujiyama, A., Hattori, M., Toyoda, A., Totoki, Y., Watanabe, H. and Sakaki, Y. BAC end sequences of Library RPCI-43
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            CGCAGAAGGCGCCCACGAGGACCCCCAGTGCCCGACGTTGCCACGGTTCTGGGATCAGAGG
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                                                                                                                                                                                                                                                                                                                                                             GCGGGGGGGGGGSKCGGSSGCSGGCGGSGGCGCGSCGCCGSCGCGGCGSCAR
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       Mus
Mus
                                  BU502934 1143
AGENCOURT_8929661 NIH_MGC_94
5', mRNA sequence.
BU502934 BU502934 GI:22808397
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Tel:81-45-503-9111, Fax:81-45-503-9170)
Clones are derived from the chimpanzee BAC library RPCI-43 This BAC end was generated during the R&D process and may have higher chance of clone tracking errors.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Sequencing: TJ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Similarity
                                                                                                                                                                                                                                                                                                                                                                                CAGGGACCAGGGAACTGCGCCCCCGCCCCTGCCCTGGCGCGAGGGAAGCT 180
                                                                                                                                                                                                                                                                                                                                                                                                         CCGGGTATAAGAAGCCTCGTGGC
                                                                                                                                                                              GGGCACGGGCTTCCCAGGGCCCGCCGGCCGCAGGAAGTTGGCCCAGGGCACGGCCGTG
                                                                                                                                                                                                                                               CTCTCTCAGAGGGCCCCAGCGCTGCCAAGAGGGAAGTCCTCGAGGCCCGGGCAGGGAAGG
                                                                                                                                                                                                                                                                                                                                                                     CGGCCGGGGAGGCGGGAGTGAGGCCTGATCGTCCCTGGCGCCTCCACCTCCCCAGG
                                                                                                                                                                  CGCAGAAGGCGCCCACGAGGACCCCCAGTGCCCGACGTTGCCACGGTCTGGGATCAGAGG
                                                                                                                          ACCACAACAACAAGAGTCGACGC
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     musculus
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R.Site
R.Site
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445 c 468 g 31 t 96 others
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Location/Qualifiers
1. .1085
                (house mouse)
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: ECORI
: ECORI.
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                                                                 bp
Mus
                                                                 musculus
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linear | DNA clone

EST 12-SEP-2002 EIMAGE:6489733

480

992 420 932 360 872 300 812 240 752

1052

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REFERENCE
AUTHORS
TITLE
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Best Local Similarity
Matches 265; Conserv
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NIH-MGC http://mgc.nci.nih.gov/.

National Institutes of Health, Mammalian Gene Collection (MGC)

L Unpublished
Contact: Robert Strausberg, Ph.D.

Email: cgapbs-@mail.nih.gov
Tissue Procurement: The Cepko Laboratory
CDNA Library Preparation: Life Technologies, Inc.
CDNA Library Preparation: Life Technologies, Inc.
CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Agencourt Bioscience Corporation
Clone distribution: MGC clone distribution information can be
found through the I.M.A.G.E. Consortium/LLNL at:
http://mage.llhl.gov
Plate: LLAM14038 row: g column: 14
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                                                                                                                                                                                                                 GGGTATAAGAAGCCTCGTGGCCTTGCCCGGGCAGCCGCAGGTTCCCCGCGCGCCCCCAGC
                                                                                        CGGAGCGGCAGGCTTTCTCAGGAGCCCGGCCGAGGCCGGCGCTGGAGGGCCGAGGACC 482
                                                                                                                                         CACGGGCTTCCCAGGGCCGCCGGCCGCAGCAGGAAGTTGGCCAGGGCACGGCC-GTGAG 422
                                                                                                                                                                                                                                                 TCTCAGAGGGCCCCCAGCGCCCAAGAGGAAGGTCCTCGAGGCCCGGGCCAGGGAAGGGGG 363
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         GCCCACGAGGACCCCCAGTGCCCGACGTTGCCACGGTCTGGGATCAGAGGCAG---GGACC 128
                                                                     e: LLAM14038 row: g column: quality sequence stop: 353.
Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         /organism="Mus musculus"
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/site_2: Sali; Cloned unidirectionally; oligo-dT primed.
Average insert size 3.3 kb. Library enriched for
full-length clones and constructed by Life Technologies.
Note: this is a NIH_MGC Library."
52 a 524 c 447 g 59 t 61 others
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       13.1%; Score 72.2; DB 13; Length 1143; 48.3%; Pred. No. 0.00065; tive 0; Mismatches 276; Indels 8;
                                                                                                                                         724
                                                                   664
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Db	Qy
603	543
cccceecc	CCCCGCGCC
595	551

Search completed: September 20, 2003, 01:39:06 Job time: 2449.79 secs